

| Application No. | Filing Date (dd/mm/yy) | Status<br>(Patented, Pending, Abandoned) |
|-----------------|------------------------|--|
| (U.S.S.N.)      | 19/05/00               | Pending                                  |
| 09/574,454      |                        | Pending                                  |
| 09/540,217      | 31/03/00               | Pending                                  |
| 09/649,167      | 23/08/00               | Pending                                  |
| 09/552,929      | 04/18/00               |  |
|                 | 26/01/01               | Pending                                  |
| 09/770,160      | 08/11/01               | Pending                                  |
| 10/014,487      | 21/11/01               | Pending                                  |
| 09/989,660      |                        | Pending                                  |
| 09/577,408      | 18/05/00               |  |

2. Specification (Total pages: 10966) consisting of:

Specification (10959 pages); Claims and Abstract (7 pages);

- 2 CD-ROMs (Tables 2-4, 6, 8-22);
- (one original and one backup)
- 0 Sheets of Drawings;

In accordance with 37 CFR 1.58 (e)(4) Applicants state that copy 1 and copy 2 of the enclosed CD-ROM discs are identical.

- Declaration and Power of Attorney (unexecuted, 7 pages);
- Request to transfer sequence listing (2 pages);
- Non-publication request (1 page);
- 6. Fee Calculation

TABLE 2: Nearest Neighbor (BlastN v. Genbank?)

|     | ACCESSION   | DESCRIPTION  | SMITH-WATERMAN<br>VALUE | % HOMOLOGY |  |
|-----|-------------|--|-------------------------|------------|--|
|     | ACCESSION   |  | ******                  |            |  |
| :   |             | Fugu rubripes putative protein 2   | 677                     | 62.195     |  |
| -   | AF026198    | Fugu rubines putative process 2  | 1685                    | 82.524     |  |
|     | AJ242724    | Homo sapiens putative mitogen-activated protein kinase kinase kinase               |                         |            |  |
| - 1 |             | Homo sapiens hypothetical protein  | 2042                    | 99.385     |  |
|     | AL117567    | Homo sapiens ATP-binding cassette protein  | 470                     | 98.701     |  |
|     | U18237      | Homo sapiens clCK0721Q.3 (Kinesin related  | 4347                    | 99.110     |  |
|     | AL021366    | protein)   |                         | 100,000    |  |
|     |             | Homo sapiens cytochrome P-450  | 3275                    | 100.000    |  |
|     | D00173      | Mus musculus HCNGP   | 1902                    | 95.130     |  |
|     | X68061      | Homo sapiens similar to mago nashi   | 968                     | 100.000    |  |
|     | AF035940    | Homo sapiens similar to mage   | 2526                    | 99.467     |  |
| )   | AC005783    | Homo sapiens R33083_1  | 5341                    | 100.000    |  |
| 10  | AB014599    | Homo sapiens KIAA0699 protein  | 1751                    | 98.496     |  |
| 11  | AL050069    | Homo sapiens hypothetical protein  | 1681                    | 99.174     |  |
| 12  | AF132963    | Homo sapiens CGI-29 protein  |                         | 95.110     |  |
| 13  | AF134983    | Mus musculus energy-dependent regulator  | 3930                    |            |  |
| 13  | ALTSTAGE    | of proteolysis   | 2748                    | 100.000    |  |
| 14  | AF100753    | Homo sapiens ancient ubiquitous 46 kDa<br>protein AUP1                             |                         |            |  |
| •   |             | Homo sapiens serine/threonine kinase   | 6047                    | 99.888     |  |
| 15  | AB015982    | Homo sapiens serine dilegen  | 181                     | 96.429     |  |
| 16  | M64229      | Homo sapiens type I collagen   | 308                     | 29.834     |  |
| 17  | Z81037      | Caenorhabditis elegans predicted using<br>Genefinder; Weak similarity in N-terminu | s                       |            |  |
|     |             |  |                         |            |  |
|     |             | FMRI :714323 comes from uns gene   | 7) 449                  | 49.624     |  |
| 18  | M35522      | Canis familiaris GTP-binding protein (rab  | 200                     | 65.000     |  |
| 19  | U40952      | Caenorhabditis elegans C03B1.10 gene   | 200                     |            |  |
| 17  | 3.5.22      | product  | 128                     | 34.211     |  |
| 20  | AJ131395    | Mus musculus collagen type XIV   | 2577                    | 100.000    |  |
| 21  | AB023210    | Homo sapiens KIAA0993 protein  | 3373                    | 99.793     |  |
| 22  | M64983      | Homo sapiens fibrinogen beta chain   | 978                     | 100.000    |  |
| 23  | D88010      | Homo sapiens ribosomal protein S13   | 433                     | 34,211     |  |
|     |             | Homo sapiens CGI-90 protein  |                         | 47.328     |  |
| 24  |             | Drosophila melanogaster actin-related  | 1269                    | 77.325     |  |
| 25  | LZ3314      | protein  | 1278                    | 64.260     |  |
| 26  | M83104      | Bos taurus cytochrome b-5 reductase  | 4179                    | 96.546     |  |
| 27  |             | Homo sapiens F23269_2  |                         | 100,000    |  |
| 1 _ |             | Homo sapiens non-histone chromosoma  | al 601                  |            |  |
| 28  | 5   0703-77 |  |                         |            |  |

|      |              | CEC/2 protoin  | 4827     | 99.212  |
|------|--------------|--|----------|---------|
| 904  | AJ011779     | Homo sapiens SEC63 protein   | 3469     | 99.590  |
| 905  | X78933       | Homo sapiens zinc finger protein   | 170      | 34.400  |
| 906  | X01655       | Homo sapiens type III procollagen (aa 892-<br>1023)                            | ****     | 99,345  |
| 907  | AF105332     | Homo sapiens vitamin D3 receptor interacting protein                           | 9085     |         |
|      |              | Homo sapiens NY-REN-55 antigen   | 4902     | 96.370  |
| 908  | AF155113     | Homo sapiens dJ55C23.1 (vanin 1)   | 3411     | 100.000 |
| 909  | AL032821     | Homo sapiens growth hormone receptor   | 4282     | 99.843  |
| 1910 | X06562       | (AA 1-638)   | 12358    | 99.545  |
|      | 10101        | Homo sapiens non-muscle myosin B   | 12021    | 41.176  |
| 1911 | M69181       | Hydra sp. mini-collagen  | 215      | 98.000  |
| 1912 | X61046       | Homo sapiens precursor   | 900      |         |
| 1913 | X51798       | Homo sapiens precursor  Homo sapiens beta glucuronidase isoform d              | 145      | 60.465  |
| 1914 | AF084256     | Homo sapiens protocadherin alpha 11  | 5459     | 89.053  |
| 1915 |              | Homo sapiens putative progesterone   | 939      | 90.955  |
| 1916 | Y12711       | binding protein  | 6743     | 99.415  |
| 1917 | AB002330     | Homo sapiens KIAA0332  | 3294     | 96.731  |
| 1918 | AF083419     | Homo sapiens calcium/calmodulin-<br>dependent protein kinase II beta e subunit | :        | 99.706  |
|      | AB020649     | Homo sapiens KIAA0842 protein  | 6825     | 75.758  |
| 1919 |              | unital a sclerosis associated retrovirus                                       | 297      | 73.730  |
| 192  | 0 A 125000   | element unknown protein 03/1   | 8346     | 99.692  |
| 192  | 1 AB002306   | Homo sapiens KIAA0308  Homo sapiens DNA polymerase alpha-                      | 9630     | 99.183  |
| 192  | 2 X06745     | l subunit (AA 1 - 1462)  |          | 99.567  |
| 192  | 23 AF028827  | Homo sapiens Tax interaction protein 40  | 1520     | 95,336  |
| 1    |              | Homo sapiens FUS gycline rich protein  | 3601     | 99.580  |
| 19:  |              | Homo sapiens similar to yeast adenylate  | 3034     | 77.380  |
| 19   | 25 000707    | cyclase (5567/6)   | 4708     | 99.864  |
| 19   | 26 AF093250  | Homo sapiens P38IP Homo sapiens CGI-119 protein                                | 1545     | 99.598  |
| 19   | 27 AF151877  | Homo sapiens gamma-aminobutyric acid   | I A 3150 | 99.786  |
| 19   | 928 AF165124 | receptor gamma 2   |          |         |

TABLE 3: Nearest neighbor (FastA v. Genbank, Genpept release 114)

|        | TABLE     | 3: Nearest neighbor (FastA v. Genbank, Genpept re  |          | %<br>IDENTITY |
|--------|-----------|--|----------|---------------|
| SEQ    | ACCESSION | DESCRIPTION  | WATERMAN | IDENTITE      |
| ID NO. |           | 1  | SCORE    |               |
| NO.    |           |  |          |               |
| NO.    |           | - intage   | 253      | 32.129        |
|        | L27428 I  | Homo sapiens reverse transcriptase   | 167      | 50.794        |
| 1      |           |  | 1001     | 56.122        |
| 2      |           |  | 164      | 25.217        |
| 3      |           |  | 320      | 26.144        |
| 4      | U17247    | Saccharomyces cerevisiae mal5, stal, Saccharomyces cerevisiae mal5, stal,                          | 524      | 1 1           |
| 5      |           |  |          |               |
|        |           | GLUCOAMYLASE S1 (EC 3.2.1.3)   | 330      | 46.774        |
|        |           |  | 265      | 49.398        |
| 6      |           |  |          | 40.865        |
| 7      |           |  | 458      | 78.571        |
| 8      | M12140    | Homo sapiens mariner transposase   | 545      | 81.818        |
| 9      | U49974    |  | 588      | 65.789        |
| 10     | AB014549  | Mus musculus Pro-Pol-dUTPase polyprotein   | 266      |               |
| 11     | Y12713    | Mus musculus Pro-Pol-dollado Fall  | 1527     | 65.445        |
| 12     | AB007903  |  | 465      | 65.979        |
|        | X78933    |  | 276      | 63.158        |
| 13     | AF081111  |  | 178      | 46.341        |
| 14     | AF081111  | Mag muggulus domesticus onti   | 271      | 49.485        |
| 15     | AB012223  |  | 222      | 43.902        |
| 16     |           |  | 870      | 71.491        |
| 17     | X03725    | Tar appiens mariner transposer   | 476      | 67.391        |
| 18     | U49974    | Trans canieng UZAFI-RS2  | 261      | 58.750        |
| 19     | D49677    |  | 295      | 50.000        |
| 20     | AJ001714  | Homo sapiens putative p150   |          | 43.434        |
| 21     | U93572    | Canis familiaris ORF2  | 182      | 40.230        |
| 22     | AB012223  |  | 176      | 35.714        |
| 23     | X53581    | Homo sapiens reverse transcriptase   | 223      | 65.574        |
| 24     | L27428    | Homo sapiens reverse crans   | 227      | 52.542        |
| 25     | 1193568   | Homo sapiens retailed pt 150  Homo sapiens putative p150  Mus musculus Pro-Pol-dUTPase polyprotein | 285      |               |
| 26     | Y12713    | Mus musculus Pro-Poi-dorrass p   | 252      | 42.149        |
| 27     | AF003535  | Mus musculus Pro-Portal Homo sapiens ORF2-like protein   | 549      | 84.821        |
|        | AF123881  | Thinle golerosis associated  |          |               |
| 28     | 12.22.000 | element gag polyprotein  | 391      | 62.500        |
| 1-0    | AF123881  | Thinle eclerosis associated associated   |          |               |
| 29     | AFIZIOU   | element gag polyprotein  | 151      | 35.294        |
| -      | AB022046  |  |          |               |
| 30     | AB022040  |  | 265      | 32.950        |
| -      | AF015539  |  |          | 57.983        |
| 31     |           | Mytilus edulis precollagem  Mus musculus Pro-Pol-duTPase polyprotei                                | 930      | 37.174        |
| 32     |           |  | 1        |               |
| 33     | AL032660  | Cenefinder   | 2666     | 88.565        |
| _      |           | 2 31iv   | 523      | 72.656        |
| 34     | AJ005073  |  |          | 33.333        |
| 35     |           | 7 Homo sapiens na  | 190      | 47.107        |
| 36     |           | Homo sapiens p40 Homo sapiens ORF2, encodes a reverse  | 248      | 14,.10,       |
| 3      |           | Homo sapiens Okrz, encour  |          | 40.206        |
| 1      |           |  | 159      |               |
| 3      | M34651    | Pseudorabies virus ORF-3 protein   | 271      | 51.724        |
| 3      |           |  | 382      | 68.31         |
|        |           | Homo sapiens DNA polymerase alpha-<br>subunit (AA 1 - 1462)  |          |               |
|        | 0 X06745  | (22.1 - 1462)  |          |               |

|       |          | Rattus norvegicus enhancer-of-split and hairy-   | 529  | 98.718 |
|-------|----------|--|------|--------|
| 10284 | AF009329 | related protein 1  | 267  | 37.725 |
| 10005 |          | the same of the sa | 237  | 85.714 |
| 10285 | L15309   | Homo sapiens zinc finger protein   | 302  | 55.000 |
| 10287 | Z98596   | Homo sapiens zinc finger protesm<br>Schizosaccharomyces pombe putative SMC family  |      | - 535  |
| 1020  |          | protein Mesocricetus auratus guanine nucleotide-   | 362  | 53.636 |
| 10288 | U13152   |  | 173  | 35,200 |
|       |          | Saccharomyces cerevisiae Msn5 protein  | 11/3 | 130    |
| 10289 | X93302   | Saccharomycos  |      |        |

TABLE 4

| TISSUE ORIGIN  RNA SOURCE  LIBRARY NAME  ABJOOL  ABJOO |             |             |        | I ADLE 4  |
|--|-------------|-------------|--------|---|
| TISSUE ORIGIN  AB3001  adult brain  GIBCO  AB3001  12 90 158 166 185 187-188 190 195 208-209 225  227 240 260 270 315 338 396 400-401 457 594  227 240 260 270 315 338 396 400-401 457 594  246 40-641 654 692 714 740 786 835 849 852 867  905 942 983 1066 1076 1087 1102 1107 1289 1302  1317 1464 1492 1679 1749 1822-1823 1846 1927  13945 2039 2164 2217 2372 2384 2448 2818 2820  2823 2834-2835 2862 2877-2878 2884 2891 2896  2996 2914 2918-2919 2932 2950 2967 2973 2978  2983 2997 3003 3010 3012-3013 3045 3066 3068  3091 3094 3110 3130-3133 1315 3165 3183 3213-  3091 3094 3110 3130-3133 1315 3165 3183 3213-  314 3223 3240 3247 3257 3260 3265 3276 2284  3312 3327 3331 3863 3341 3427 3441 3448  3453 3461 3465 3469 3471 3492 3499 3506 3508  3515 3534 3536 3542-3543 3593 3566 363 3666 3668 3683  3631-3632 3638 3646 3655 3663 3666 3668 3683  3631-3632 3638 3646 3655 3663 3666 3668 3683  3631-3632 3638 3646 3655 3663 3666 3668 3683  3631-3632 3638 3646 3655 3663 3666 3668 3683  3636 3693 3740 3745 7347-3748 3758 3762 3779  3782-3783 3866 3871-3872 3877 3919 3943-3944  3985 3978 3994 3996 4000 4006 4008 4010 4036  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4106  4040 4043 4057 4060 4068 4074 4093 4097 4098  4044 4947 4252 4254 4256 4257 4258 4258 4258 4258 4258 4258 4258 4258  |             |             |        | GRO ID NOS:                                       |
| ORIGIN NAME  LIBRANY ORIGIN  ABJOOL  ABJOOL  ABJOOL  ABJOOL  12 90 158 166 185 187-188 190 195 208-209 225 400-401 457 594 6646-641 654 692 714 740 786 835 849 852 867 640-641 654 692 714 740 786 835 849 852 867 640-641 654 692 714 740 786 835 849 852 867 905 942 983 1066 1076 1087 1102 1107 1289 1302 1317 1464 1492 1679 1749 1822-1823 1846 1927 1347 1464 1492 1679 1749 1822-1823 1846 1927 1347 1464 1492 1679 1749 1822-1823 1846 1927 1296 293 2934 2934 2285 22877-2878 2884 2849 2820 2283 22834-2835 2862 2877-2878 2884 2849 2830 2936 2937 3073 3010 3012-3013 3045 3066 3068 2983 2937 3003 3010 3012-3013 3045 3066 3068 3069 3091 3094 3110 3130-3131 3135 3155 3183 3213-3091 3094 3110 3130-3131 3165 3183 3213-3091 3094 3120 3327 3331 3381 3395 3411 3427 3441 3448 3312 3327 3331 3381 3395 3411 3427 3441 3448 3312 3327 3331 3381 3395 3411 3427 3441 3448 3312 3327 3331 3381 3395 3411 3427 3441 3448 3453 3461 3465 3469 3471 3492 3499 3505 308 3653 3631-3632 3666 3673 3666 3663 3663 3668 3683 3631-3632 3686 3693 3740 3745 3747-3748 3758 3762 3779 37882-3783 3866 3871-3872 3877 3919 3943-3944 3782-3783 3866 3871-3872 3878 3996 4000 4006 4008 4001 4003 4007 4004 4004 4004 4004 4007 4007  |             | TATA COURCE | HYSEO  | SEQ ID NOO!                                       |
| adult brain GIBCO AB3001 12 90 158 166 185 187-188 190 195 2008-209 225 227 240 260 270 315 338 396 400-401 457 594 640-641 654 692 714 740 786 835 849 852 867 640-641 654 692 714 740 786 835 849 852 867 905 942 983 1066 1076 1087 1102 1107 1289 1302 1317 1464 1492 1679 1749 1802-1823 1846 1927 1347 1464 1492 1679 1749 1802-1823 1846 1927 1345 2095 2914 2918-2919 2932 2950 2967 2973 2978 2965 2914 2918-2919 2932 2950 2967 2973 2978 2962 2914 2918-2919 2932 2950 2967 2973 2978 2962 2914 2918-2919 2932 2950 2967 2973 2978 2963 2997 3003 3010 3012-3013 3045 3066 3068 2983 2997 3003 3010 3012-3013 3045 3066 3068 3141 3427 3423 3427 3223 3240 3247 3257 3260 3265 3276 3284 3312 3327 3321 3381 3395 3341 3427 3441 3448 3312 3327 3321 3381 3395 3351 3593 3563 3663 3663 3663 3663 3663 3663   |             | RNA SOURCE  |        |   |
| 227 240 260 270 315 38 30 50 54 57 67 67 640-641 654 692 714 740 786 335 849 852 867 640-641 654 692 714 740 786 335 849 852 867 905 942 983 1066 1076 1087 1102 1107 1289 1302 1317 1464 1492 1679 1749 182-1823 1846 1927 1945 2039 2164 2217 2372 2384 2448 2818 2820 2823 2834-2835 2862 2877-2878 2884 2881 2896 2823 2834-2835 2862 2877-2878 2884 2881 2896 2962 2914 2918-2919 2932 2950 2967 2973 2978 2963 2997 3003 3010 3012-3013 3045 3066 3068 3091 3094 3110 3130-3131 3135 3165 3183 3213-31091 3094 3110 3130-3131 3135 3165 3183 3213-312 327 3331 3381 3393 3411 3427 3441 3448 3312 3327 3331 3381 3393 3411 3427 3441 3448 3312 3327 3331 3381 3393 3411 3427 3441 3448 3312 3327 3331 3364 3465 3465 3663 3663 3663 3683 3631-3622 3638 3646 3655 3663 3666 3668 3683 3631-3622 3638 3646 3655 3663 3666 3668 3683 3631-3622 3638 3646 3655 3663 3666 3668 3683 3631-3872 3877 3919 3943-3944 3965 3978 3984 3996 4000 4006 4008 4010 4036 4040 4043 4057 4060 4068 4074 4093 4097 4106 4040 4043 4057 4060 4068 4074 4093 4097 4106 4024 4024 4224 4224 4224 4224 4224 42   | ORIGIN      |             |        | 205 208-209 225                                   |
| 227 240 260 270 315 38 30 50 54 57 67 67 640-641 654 692 714 740 786 335 849 852 867 640-641 654 692 714 740 786 335 849 852 867 905 942 983 1066 1076 1087 1102 1107 1289 1302 1317 1464 1492 1679 1749 182-1823 1846 1927 1945 2039 2164 2217 2372 2384 2448 2818 2820 2823 2834-2835 2862 2877-2878 2884 2881 2896 2823 2834-2835 2862 2877-2878 2884 2881 2896 2962 2914 2918-2919 2932 2950 2967 2973 2978 2963 2997 3003 3010 3012-3013 3045 3066 3068 3091 3094 3110 3130-3131 3135 3165 3183 3213-31091 3094 3110 3130-3131 3135 3165 3183 3213-312 327 3331 3381 3393 3411 3427 3441 3448 3312 3327 3331 3381 3393 3411 3427 3441 3448 3312 3327 3331 3381 3393 3411 3427 3441 3448 3312 3327 3331 3364 3465 3465 3663 3663 3663 3683 3631-3622 3638 3646 3655 3663 3666 3668 3683 3631-3622 3638 3646 3655 3663 3666 3668 3683 3631-3622 3638 3646 3655 3663 3666 3668 3683 3631-3872 3877 3919 3943-3944 3965 3978 3984 3996 4000 4006 4008 4010 4036 4040 4043 4057 4060 4068 4074 4093 4097 4106 4040 4043 4057 4060 4068 4074 4093 4097 4106 4024 4024 4224 4224 4224 4224 4224 42   |             |             |        | 12 90 158 166 185 187-188 190 195 208-205 225     |
| 640-641 654 692 714 740 7.00 1107 1289 1302 905 942 983 1066 1076 1087 1102 1107 1289 1302 1317 1464 1492 1679 1749 1822-1823 1846 1927 1317 1464 1492 1679 1749 1822-1823 1846 1927 1345 2019 2164 2217 2372 2384 2448 2818 2820 2823 2834-2835 2862 2877-2878 2884 2891 2896 2829 2997 3003 3010 3012-3013 3045 3066 3068 2983 2997 3003 3010 3012-3013 3045 3066 3068 2983 2997 3003 3010 3012-3013 3045 3066 3068 2983 2997 3003 3010 3012-3013 3045 3066 3068 2913 2924 3227 3257 3260 3265 3276 3284 3312 3327 3331 3381 3395 3411 3427 3441 3448 3312 3327 3331 3381 3395 3411 3427 3441 3448 3312 3327 3331 3381 3395 3411 3427 3441 3448 3453 3461 3465 3469 3471 3492 3499 3506 3638 3631 3633 3638 3646 3655 3663 3663 3668 3683 3631 3633 3638 3646 3655 3663 3666 3668 3683 3631 3639 3740 3745 3747-3748 3758 3762 3779 3782-3783 3866 3871-3872 3877 3919 3943-3944 3965 3978 3994 3996 4000 4006 4008 4010 4036 4040 4043 4057 4060 4068 4074 4093 4097 4106 4040 4043 4057 4060 4068 4074 4093 4097 4106 4040 4043 4057 4060 4068 4074 4093 4097 4106 4043 4134 4145 4150 4178 4193 4228 4244 4247 4247 4247 4248 4247 4247   | adult brain | GIBCO       | AB3001 | 227 240 260 270 315 338 396 400-401 457 594       |
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| 4944 4947 4968 491, 4988 491, 4988 591, 5126 5132 5136 5098 5112 5115 5120-5121 5124 5126 5132 5136 5098 5112 5115 5170-5121 5127 5189 5196 5199 5216 5235 5259 5163 5171 5177 5189 5196 5199 5216 5235 5259 5289 5292 5294 5298 5396 5882 5403 5415 5443 5450 5459 5462 54618 5618 5622 5624 5563 5563 5563 5563 5667 5661 56618 5622 5624 5663 5563 5565 5667 5661 56618 5662 5703 5627 5645 5651 5663 5667 5681 5698 5700 5703 5718 5720 5733-5735 5764 5775 5787-5788 5791 5796 5800 5804 5804 5824 5825 5832 5842 5863 5668 5896 5805 5804 5804 5804 5824 5825 5832 5842 5863 5668 5896 5897 5908 5921 5929 5950 5961 5974 6032 6039-6040 6051 6057 6067 6069 6078 6096 6100 6105 6114 6131 6134 6143 6143 6143 6145 6153 6157 6168 6176 6186 6192 6204 6211 6216 6222 6224 6224 6230 6232-6236 6236 6236 6236 6236 6236 6236   | 1           | 1           | 1      | 4000 4899 4912 4917-4918 4929-4930 4935 4940      |
| 5098 5112 5115 5120-5121 5196 5199 5216 5235 5259 5163 5171 5177 5189 5196 5199 5216 5235 5259 5163 5171 5177 5189 5196 5199 5216 5235 5259 5279 5289 5292 5294 5298 5376 5382 5403 5415 5433 5455 5459 5462 5469 5476 5540 5551 5554 5563 5582-5583 5589 5596 5512 5618 5622 5624 5563 5582-5583 5589 5596 5512 5618 5622 5624 5651 5663-3-567 5681 5698 5700 5703 5718 5720 5733-5735 5764 5775 5787-5788 5791 5718 5720 5733-5735 5764 5775 5787-5788 5791 5718 5720 5733-5735 5764 5775 5787-5788 5791 5786 5800 5804 5824-5825 5832 5842 5863 5868 5796 5800 5804 5824-5825 5832 5842 5863 5868 5796 5800 5804 5824-5825 5832 5842 5863 6039-6040 6051 6057 6067 6069 6078 6096 6100 6105 6105 6114 6131 6134 6143 6145 6136 6137 6168 6176 6118 6192 6204 6211 6216 6222 6226-6230 6232-6236 6232 6236 6231 6232 6232 6236 6231 6232 6232  |             |             | 1      | 4888 4057 4968 4971 4989 4998 5026 5063 5096      |
| \$163 \$171 \$177 \$189 \$189 \$180 \$382 \$403 \$415 \$279 \$289 \$292 \$294 \$298 \$376 \$382 \$403 \$415 \$279 \$289 \$272 \$298 \$376 \$582 \$403 \$415 \$243 \$5450 \$459 \$462 \$469 \$476 \$540 \$551 \$554 \$543 \$5563 \$582 \$582 \$582 \$582 \$582 \$582 \$582 \$582  | 1           | 1           | 1      | 4944 4947 1315 5120-5121 5124 5126 5132 5136      |
| 5279 5289 5292 5294 5296 5540 5550 5551 5554 5450 5451 5554 5450 5455 5455   | 1           |             | 1      | 5098 5112 5113 5126 5196 5199 5216 5235 5259      |
| 5443 5450 5459 3462 3462 3462 3462 5626 5624 5563 5582-5583 5582 5583 5589 5596 5512 5618 5622 5624 5563 5582-5583 5589 5596 5512 5618 5622 5624 5625 5645 5651 5663 5687 5500 5703 5627 5645 5651 5663 5667 5706 5703 5718 5726 5735 5736 5764 5775 5787-5788 5791 5718 5796 5800 5804 5824-5825 5832 5842 5863 5868 5796 5807 5807 5807 5807 5607 6067 6069 5906 6000 6100 6105 6007 6005 6007 6007 6009 6000 6100 6105 6007 6007 6007 6007 6009 6000 6100 6105 6114 6131 6134 6143 6145 6153 6157 6168 6176 6188 6192 6220 6216 6226 6226 6230 6232-6238 6232 6232 6232 6232 6232 6232 6232   | 1           |             | 1      | 5163 51/1 51/7 5100 5298 5376 5382 5403 5415      |
| 5563 5582-5583 5582 5581 5698 5700 5703 5627 5645 5651 5663-5667 5681 5698 5700 5703 5718 5720 5733-5735 5764 57575 5787-5788 5791 5718 5720 5733-5735 5764 575 5787-5788 5791 5796 5800 5804 5804 5824-5825 5832 5842 5863 5868 5897 5908 5921 5929 5996 5961 5974 6032 6039- 6040 6051 6057 6067 6069 6078 6096 6100 6040 6051 6057 6067 6069 6078 6096 6100 6114 6131 6134 6143 6145 6153 6157 6168 6176 6118 6192 6204 6211 6216 6222 6223 6232- 6233 6252 6263 6280-6281 6285 6292 6296 6313 6331 6332 6325 6327-6328 6330 6332-6334 6336- 6331 6334 6335-6356 6384 6391-6392 6407 6414 6416-6417 6422 6448 6456 6459 6480 6491 6502 6416-6417 6422 6448 6456 6459 6480 6491 6502 6507-6508 6512 6517 6522 6525 6534 6538 6541 6547-6548 6553 6562-6666 6572 6575 6610 6618 6547-6548 6553 6562-6666 6572 6575 6610 6618  |             | 1           |        | 5279 5289 5292 5254 5476 5540 5551 5554           |
| 5627 5645 5651 5663-5667 5764 5775 5787-5788 5791 5718 5720 5733-5735 5764 5775 5787-5788 5791 5718 5720 5733-5735 5764 5775 5787-5788 5791 5800 5800 5804 5824-5825 5832 5842 5863 5868 5796 5800 5804 5824-5825 5832 5842 5863 5868 5897 5908 5921 5950 5961 5974 6032 6039- 6040 6051 6057 6067 6069 6078 6096 6100 6105 6114 6131 6134 6143 6145 6153 6157 6168 6176 6118 6192 6204 6211 6216 6222 6226-6230 6232- 6188 6192 6203 6280-6281 6285 6292 6296 6131 6233 6252 6263 6280-6281 6285 6292 6296 6131 6321 6323 6325 6337-6328 6330 6332-6334 6336- 6337 6343 6355-6356 6384 6391-6392 6407 6414 6337 6343 6355-6356 6384 6391-6392 6407 6414 6347 6422 6448 6456 6459 6400 6491 6502 6416-6417 6422 6448 6456 6459 6400 6491 6502 6416-6477 6548 6553 6562-6563 6572 6575 6610 6618 6547-65548 6553 6562-6563 6572 6575 6610 6618  |             | 1           | 1      | 5443 5450 5459 5462 5403 5612 5618 5622 5624      |
| 5718 5720 5733-5735 5762 5832 5842 5863 5868<br>5796 5800 5804 5824-5825 5832 5842 5863 5868<br>5897 5908 5921 5929 5950 5951 5974 6032 6039-<br>6040 6051 6057 6067 6069 6078 6096 6100 6105<br>6114 6131 6134 6143 6145 6153 6157 6168 6176<br>6188 6192 6204 6211 6216 6222 6226-6230 6232-<br>6233 6252 6263 6280-6281 6285 6292 6296 6313<br>6321 6323 6325 6327-6328 6330 6332-6334 6336-<br>6337 6343 6355-6356 6384 6391 6-392 6407 6414<br>6337 6345 6355-6356 6384 6391 6-392 6407 6414<br>6416-6417 6422 6448 6456 6459 6480 6491 6502<br>6416-6417 6422 6448 6456 6459 6480 6491 6502<br>6507-6508 6512 6557 6552 6557 6575 6610 6618<br>6597-6598 6553 6562-6666 6572 6575 6610 6618  |             |             | 1      | 5563 5582-5583 5589 5390 5622 5698 5700 5703      |
| 5718 5720 5733-5735 5762 5832 5842 5863 5868<br>5796 5800 5804 5824-5825 5832 5842 5863 5868<br>5897 5908 5921 5929 5950 5951 5974 6032 6039-<br>6040 6051 6057 6067 6069 6078 6096 6100 6105<br>6114 6131 6134 6143 6145 6153 6157 6168 6176<br>6188 6192 6204 6211 6216 6222 6226-6230 6232-<br>6233 6252 6263 6280-6281 6285 6292 6296 6313<br>6321 6323 6325 6327-6328 6330 6332-6334 6336-<br>6337 6343 6355-6356 6384 6391 6-392 6407 6414<br>6337 6345 6355-6356 6384 6391 6-392 6407 6414<br>6416-6417 6422 6448 6456 6459 6480 6491 6502<br>6416-6417 6422 6448 6456 6459 6480 6491 6502<br>6507-6508 6512 6557 6552 6557 6575 6610 6618<br>6597-6598 6553 6562-6666 6572 6575 6610 6618  | 1           |             | 1      | 5627 5645 5651 5663-5667 5681 5090 5787-5788 5791 |
| 5796 5800 5804 5824-3625 5950 5961 5974 6032 6039- 5897 5908 5921 5929 5950 5961 5974 6032 6039- 6040 6051 6057 6067 6069 6078 6096 6100 6105 6114 6131 6134 6143 6145 6153 6157 6168 6176 6188 6192 6204 6211 6216 6222 6226-6220 6232- 6188 6192 6204 6211 6216 6222 6226-6220 6232- 6233 6252 6263 6280-6281 6285 6292 6296 6313 6321 6323 6325 6327-6328 6330 6332-6334 6336- 6337 6343 6355-6356 6384 6391-6392 6407 6414 6317 6327 6348 6455 6439 6480 6491 6502 6416-6417 6422 6448 6455 6439 6480 6491 6502 6507-6508 6512 6517 6522 6525 6534 6538 6541 6507-6508 6515 6562-6563 6572 6575 6610 6618  | · ·         | 1           | 1      | 5718 5720 5733-5735 5764 5773 5767 5863 5868      |
| 5897 5908 5921 5929 5930 6078 6096 6100 6105 6040 6051 6057 6067 6069 6078 6096 6100 6105 6105 6104 6131 6134 6143 6145 6153 6157 6168 6176 6184 6192 6204 6211 6212 6222 6226-6230 6232-6233 6252 6263 6280-6281 6285 6292 6296 6313 6326 3227-6328 6330 6332 6332 6325 6326 6384 6391-6392 6407 6414 6337 6345 6355-6356 6384 6391-6392 6407 6414 6417 6422 6448 6456 6459 6480 6491 6502 6416-6417 6422 6448 6456 6459 6480 6491 6502 6416-6476 6486 6459 6480 6491 6502 6416-6476 6486 6459 6480 6491 6502 6416-6476 6486 6459 6480 6491 6502 6416-6476 6486 6459 6480 6491 6502 6416-6477 6548 6553 6562-6563 6572 6575 6610 6618 6547-6548 6553 6562-6563 6572 6575 6610 6618 6547   |             |             | 1      | 5796 5800 5804 5824-5825 5832 5842 5000 6039-     |
| 6040 6051 6057 6067 6067 6069 6069 6176 6176 6176 6176 6174 6131 6134 6145 6153 6157 6168 6176 6184 6192 6204 6211 6216 6222 6226-6230 6232-6236 6232 6236 6236 6236 6236 6236   | 1           |             |        | 5897 5908 5921 5929 5950 5961 5974 6032 6005      |
| 6114 6131 6134 6143 6143 622 6226-6230 6232-6188 6192 6204 6211 6216 6222 6226-6230 6232-6188 6192 6204 6211 6216 6222 6226 6236 6313 6233 6252 6263 6280-6281 6285 6292 6296 6313 6321 6323 6325 6327-6328 6330 6332-6334 6336-6321 6327 6343 6355-6356 6384 6391-6392 6407 6414 6337 6345 6355-6356 6384 6391-6392 6407 6414 6417 6422 6448 6456 6459 6400 6491 6502 6416-6417 6422 6448 6456 6459 6400 6491 6502 6507-6508 6512 6517 6522 6525 6553 6534 6538 6541 6507-6508 6512 6517 6526 6536 6592 6736 6618 6547-6548 6555 6562-6563 6572 6575 6610 6618  | 1           |             |        | 6040 6051 6057 6067 6069 6078 6096 6100 6103      |
| 6188 6192 6204 6218 6218 6228 6292 6296 6313 6235 6252 6263 6280-6281 6285 6292 6296 6313 6325 6263 6280-6281 6285 6292 6296 6313 6321 6322 6325 6327-6328 6330 6332-6334 6336-633 6345 6355-6356 6348 6391-6392 6407 6414 6416-6417 6422 6448 6456 6459 6480 6491 6502 6416-6417 6422 6448 6456 6459 6480 6491 6502 6507-6508 6512 6517 6552 6525 6534 6580 6587-6598 6515 6552 6553 6573 6576 6610 6618 6547-6548 6553 6563 6573 6573 6692 6714  | 1           |             | 1      | 6131 6134 6143 6145 6153 6157 6168 6176           |
| 6233 6252 6263 6280-6261 6332 6334 6336-6332 6332 6335-6332 6325 6327-6328 6330 6332-6334 6336-6321 6323 6325-6356 6384 6391-6392 6407 6414 6337 6345 6355-6356 6384 6391-6392 6407 6418-6417 6422 6448 6456 6459 6534 6538 6541 6507-6508 6512 6517 6522 6525 6534 6538 6541 6507-6508 6553 6562-6563 6572 6575 6610 6618 6547-6548 6553 6562-6563 6572 6576 6619 6618  | 1           |             | l      | 6114 6101 6204 6211 6216 6222 6226-6230 6232-     |
| 6321 6323 6325 6327-6326 6384 6391-6392 6407 6414 6337 6345 6355-6356 6384 6391-6392 6407 6414 6337 6345 6355-6356 6384 6391-6392 6502 6416-6417 6422 6448 6456 6459 6480 6491 6502 6416-6417 6422 6448 6456 6459 6480 6491 6507-6508 6512 6517-6505 6502 6514 6538 6541 6547-6548 6553 6562-6566 6572 6575 6610 6618 6547-6548 6553 6562-6566 6572 6574 6692 6714   | 1           | 1           |        | 6188 6192 6263 6280-6281 6285 6292 6296 6313      |
| 6337 6343 6355-6336 6369 6480 6491 6502 6416-6417 6422 6448 6456 6459 6480 6491 6502 6416-6417 6422 6525 6525 6534 6538 6541 6507-6508 6512 6517 6572 6575 6610 6618 6547-6548 6553 6562-6563 6572 6575 6610 6618  | 1           | 1           | 1      | 6233 6252 6263 6227-6328 6330 6332-6334 6336-     |
| 6337 6343 6355-6336 6369 6480 6491 6502 6416-6417 6422 6448 6456 6459 6480 6491 6502 6416-6417 6422 6525 6525 6534 6538 6541 6507-6508 6512 6517 6572 6575 6610 6618 6547-6548 6553 6562-6563 6572 6575 6610 6618  |             | 1           | 1      | 6321 6323 6325 6327 6394 6391-6392 6407 6414      |
| 6416-6417 6422 6448 6450 6524 6538 6534 6538 6541 6507-6508 6512 6517 6522 6525 6534 6538 6541 6507-6548 6553 6562-6563 6572 6575 6610 6618 6547-6548 6653 6562-6563 6572 6576 6630 6618   |             | 1           | 1      | 6337 6343 6355-6356 6364 6352 6480 6491 6502      |
| 6507-6508 6512 6517 6322 6323 6610 6618<br>6547-6548 6553 6562-6563 6572 6675 6610 6618  | 1           |             | 1      | 6416-6417 6422 6448 6456 6435 6534 6538 6541      |
| 6547-6548 6553 6562-6563 6590 6692 6714  |             | 1           | 1      | 6507-6508 6512 6517 6522 6525 6534 6536 6618      |
| 6621 6624 6629 6642 6671 6684 6690 6692 6714<br>6730 6742-6744 6757 6787 6790 6797 6804-6805   |             | 1           | 1      | 6547-6548 6553 6562-6563 6572 6575 6610 6610      |
| 6730 6742-6744 6757 6787 6790 6797 6804-5805   |             | 1           | 1      | 6621 6624 6629 6642 6671 6684 6690 6692 6714      |
| 6/30 6/72 0  | 1           |             | 1      | 6730 6742-6744 6757 6787 6790 6797 6804-6803      |
|  |             |             |        | 0/30 0.42 0.22                                    |
|  |             |             |        |   |

| 8827 8876 8907 8917 8952 8963 9031-9032 9075<br>9090 9119 9151 9175 9205 9274 9349 9550 9590<br>9600 9667 9747 9839 9937 10164 | 75<br>90 |
|--|----------|
|--|----------|

TABLE 6: Nearest neighbor (FastA v. Genbank, Genpept release 114)

|      | TAB       | LE 6: Nearest neighbor (1 aser 1 . Garage   | SMITH-   | %                    |
|------|-----------|---|----------|----------------------|
|      |           | DESCRIPTION   | WATERMAN | IDENTITY             |
| ~~   | ACCESSION |   | SCORE    |                      |
| ID   | NO.       |   |          |                      |
| 10.  |           | . Nahaga  | 997      | 42.359               |
|      |           | Synechocystis sp. asparaginyl-tRNA synthetase   |          | 32.847               |
|      |           | geomorhabditis elegans product  |          |                      |
| 11   |           |   | 117      | 29.008               |
|      |           | Homo sapiens KIAA0978 protein   | 254      | 62.069               |
| 12   | AB023195  | meniane ORF1: MER3/; pucusari   |          |                      |
| 13   | U49973    |   | 189      | 23.211               |
|      |           |   | 111      | 28.182               |
| 14   | AF053091  | Drosophila melanogaster Cyses<br>Saccharomyces cerevisiae ORF YKL083w   | 245      | 37.398               |
| 15   | Z28082    | Homo sapiens p40  | 405      | 59,259               |
| 16   | U93571    | Homo sapiens F23487 2 Homo sapiens F23487 2   | 323      | 50.847               |
| 17   | AC004602  | Homo sapiens F23487 2 Peromyscus maniculatus reverse transcriptase  | 306      | 50.909               |
| 18   | บ70935    | Homo sapiens unknown protein  |          | 50.000               |
| 19   | M22334    | Homo sapiens unknown protein Mus musculus involved in signaling by the epiderm  | nal 276  | 30.003               |
| 20   | U29156    | Mus musculus involved in signating of growth factor receptor; Method: conceptual  |          |                      |
| 1    |           | translation supplied by author  | 224      | 32.215               |
| 1    |           | Ovine pulmonary adenocarcinoma virus gag  |          | 47.486               |
| 21   | A27950    | Ovine pulmonary adenocarcinoma virus Homo sapiens neuronal thread protein AD7c-NTP  | 355      | 62.195               |
| 22   | AF010144  | Homo sapiens neuronal thread protection. Homo sapiens chromatin assembly factor-I pl50  | 228      | 02.175               |
| 23   | U20979    | Homo sapiens chromatin assembly   |          | 42,647               |
| 1 23 | -         | subunit grame (196 AA)  | 112      | 29.487               |
| 24   | D00570    | subunit  Mus musculus open reading frame (196 AA)  Arabidopsis thaliana cell wall protein  Arabidopsis thaliana cell wall protein | 91       | 26.786               |
| 25   | L34685    | Arabidopsis thaliana cell wall propuglease V, bet   | a 50     | 26.786               |
| 26   | AE001164  | Borrelia burgdorieri exodeoxi   |          | 34.307               |
| 20   | 722       | chain (recB)  | 124      |                      |
| 27   | M90464    | chain (recB)  Homo sapiens alpha-5 type IV collagen  Rattus norvegicus lamina associated polypeptide                              | 1C 835   | 58.436               |
| 28   | U20286    |   | 134      | 31.000               |
| 29   | AB016092  |   | 255      | 34.016               |
| 30   | AJ24346   | 2 Homo sapiens RNA Blitching protection of Leishmania major protection frame 2  | 179      | 38.281               |
|      | X61296    |   | 219      | 57.303               |
| 31   | M22334    | Homo sapiens unknown protein  | 124      |                      |
| 32   | AL03353   | the search aromyces Donibe Seline   | 348      | 56.557               |
| 33   | U93570    | Homo sapiens putative p150  | 283      |                      |
| 34   | AF01014   | - appiens neuronal thread pro-  | 93       | 33.588               |
| 35   | Y00706    |   | 283      | 29.536               |
| 36   |           | Homo sapiens hypothetical protein   | 608      |                      |
| 37   | AL04980   | ennione ORF1: MER3/; Pucusi   | 1        |                      |
| 38   | U49973    | similar to pogo element   | 27       | 7 35.338             |
|      |           |   |          |                      |
| 39   | M13002    | start codon in ORF 2; putative  | 18       | 8 29.940             |
|      |           | start codon in ORF 2; putative 00 Haliotis discus collagen pro alpha-chain 00 Haliotis discus collagen pro protein 2              | 23       | 2 55.128             |
| 40   |           |   | 21       |                      |
| 41   |           |   | 16       |                      |
| 42   |           |   | 41       |                      |
| 43   |           |   | 10       |                      |
| 44   | M91463    | nuclear factor i  | 16       |                      |
| 4    |           |   | 20       | -                    |
| 4.0  | M22334    | Homo sapiens unknown pro-   |          | , ,                  |
| 4    |           | B Rattus norvegicus DRPLA Crithidia oncopelti NADH dehydrogenase subunit  | 5 10     | 70                   |
|      |           | Crithidia oncopelti NADA denyereges<br>877 Streptomyces collinus NapG oxidoreductase  | 1        | 51 31.44<br>50 64.23 |
| 4    |           |   |          |                      |

|      |           |   | 56    | 58.333 |
|------|-----------|---|-------|--------|
|      |           | Thermotoga maritima hypothetical protein  |       | 43.939 |
|      | AE001793  | Thermotoga maritima hypothetical product Homo sapiens ORF1 codes for a 40 kDa product Homo sapiens ORF1 codes for a 40 kDa product  | 82    | 45.161 |
| 3776 | M80344    | Homo sapiens ORF1 codes for a 40 kbs production (Caenorhabditis elegans predicted using Genefinder;   |       |        |
| 3777 |           | Preliminary prediction Archaeoglobus fulgidus A. fulgidus predicted coding  | 87    | 37.500 |
| 3778 | AE001098  | Archaeoglobus ruigidus XX<br>region AF0123<br>Erimystax dissimilis NADH ubiquinone oxidoreductase   | 84    | 32.609 |
| 3779 | AF085753  | Erimystax dissimilis NADA ubiquesis<br>subunit 2  | 95    | 38.889 |
| 3780 | U60669    | subunit 2 Homo sapiens 1,25-dihydroxyvitamin D3 24-<br>hydroxylase Homo sapiens 1,25-dihydroxyvitamin D3 24-  | 99    | 39.189 |
| 3781 | U60669    | Homo sapiens 1,25-dinydroxy   |       | 56.000 |
| J    |           | hydroxylase hydroxylase from pUC9; putative   | 106   | 45.000 |
| 3782 |           | hydroxylase vectors LacOPZ-alpha peptide from pUC9; putative vectors LacOPZ-alpha peptide from pUC9; putative Pseudomonas aeruginosa similar to E. coli protein Pseudomonas aeruginosa similar to E. coli protein Pseudomonas | 79    |        |
| 3783 | U15370    | n-in/Dina Swiss-Prot Accession  | 82    | 27.500 |
|      |           | Chlorella vulgaris ORF54d   | 1343  | 57.576 |
| 3784 |           | Chlorella vulgaris ORF540 Unknown possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST   |       |        |
| 378  | 5 U09453  | EMBL: M9115 Comes from EMBL: D715 Cricetulus griseus UDP-N-acetylglucosamine: dolichyl phosphate N-acetylglucosamine 1-phosphate  | 234   | 66.667 |
|      |           | transferase transferase SP KD   | 180   | 38.889 |
| 378  | 7 Z93386  | Unknown Similarity to Yeast hypothetical protein (SW:P43616); cDNA EST EMBL:M89432 comes fr   | 785   | 91.270 |
|      |           |   | 606   | 87.379 |
| 378  | 8 X58906  |   | 458   | 100.00 |
| 378  |           | Saccharomyces cerevisiae Ylr404wp Saccharomyces cerevisiae Ylr404wp Saccharomyces cerevisiae Ylr404wp   | 1055  | 40.000 |
| 379  |           | Saccharomyces cerevisiae Ylr404wp  Homo sapiens Similarity to Human host cell factor C1 (SW:P51610); cDNA EST yk205a3.5 comes from this   |       |        |
| L    |           | gen CFESS55F:   | 11112 | 54.493 |
| 37   | 92 U80448 | Unknown coded for by C. elegans CDNA yk84al.3; coded for by C. elegans CDNA yk84al.3; coded for by C. elegans CDNA pelicase (DEAD family)   | 2817  | 100.00 |
|      |           |   | 2437  |        |
|      | 93 Z37166 | Homo sapiens precursor polypeptide  Homo sapiens precursor polypeptide  | 1900  |        |
|      | 94 X04494 |   | 1     | 1      |
| 37   | 95 AF0158 | 111 Mus muscular page 2012 acyltransferase 2015 Homo sapiens QA79 membrane protein  | 3166  | 100.00 |
| 1-05 | D.T.0073  | 195 Homo sapiens QA79 membrane process  |       |        |

TABLE 8

|     |                |       |   |  | TABLE 8  |
|-----|----------------|-------|---|--|--|
|     |                |       |   |  | THE MICLEOTIDE   |
| D D | Me<br>th<br>od | in to | redict- d beg- nning ucleo- ide oca- corres- conding to first | acid   | AMINO ACID SEQUENCE ENCODED BY THE NUCLEOTIDE SEQUENCE OF THE CORRESPONDING SEQ ID NO. (A=Alanine, C=Cysteine, p=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, N=Asparagine, T=Threonine, V=Valine, W=Tryptophan, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)   |
|     |                |       | acid<br>residue<br>of amino<br>acid<br>sequ-                  | residue<br>of amino<br>acid<br>sequ-<br>ence |  |
|     | 1_             | ᆚ     | ence  |  | MPGPFGSLYLLLWNIPVTSSNSFHSWQGNFLKFTRNTTKRNFR*   |
| 1   |                |       | 31  | 162  | MPGPFGSLYLLLWNIPYTSSNSFHSWGGNFLKFTRNT-TRNT-TRNT-TRNT-TRNT-TRNT-TRNT-TRNT   |
| 2   | 1              | 1     | 337   | 1  | GHGLPGGPAAPWAASQWVDGVAGKET GTTTT   |
| 3   | 1              | A     | 1   | 379  | VCOCT.RPSTPSPPSPPGDPGRAGCQ1 (5 (***  |
| 4   | +              | A     | 29  | 317  | SSSYNSSSTFIYVCLFCAQSITLK/CHFBBCKLKENQGPKEG LNH*CHMYCIPKFTI*NTWLFFCRVFLFISFFELKLKENQGPKEG   |
| 5   |                | A     | 2   | 468  | RLIYVYYY*LDETMSNK\DSRNEI TOT TOT TO THE INTERPRETATION OF THE INTE |
| 6   |                | A     | 13  | 534  | IRLRSHPSPQAYPPPPVLPTGQFTCHTHAND  IRLRSHPSPQAYPPPVLPTQFTCHTHAND  LPLHPLSPLSAALSPPLXRRTPPPLLSPLLPPCQALDLAAXXLVRCGDLPQ  LSHHPOOOTPSTHDPWPL  TSHHPOOOTPSTHDPWPL  |
| 7   |                | A     | 3   | 397  | STGLAYILLTETLKLSKLSTQ\ETHERLETSUGGENKANVDQSRAEVMAMVFW<br>GLL*RTVTGDETGLFQYDPENKAQ/SKPRGSGPVKANVDQSRAEVMAMVFW<br>NAOGILLVDFLKSQRPITSAYYESIYYEK  |
| -   |                | 10    | 47  | 202  | MIKTQCYTFIPNSTAPNKSITKALQGLTALSNSSDSARAGGRHCVPFLLWDE<br>SLELLVFSLYGSWCKGDSLLEEKQKLIRPEHRRMNLAAPGGRHCVPFLLWDE<br>SLELLVFSLYGSWCKGDSLLEEKQKLIRPEHRRMNLAAPGCHCVPFLLWDE  |
| 9   |                | P     |   | 319  | WEGIKGSRVGLVWSGQV/VKEGING  |
| 10  | l              | 1     | A 667   | 1  | HTPSKDPIGAHHPGSITQMPSSGSTDVFFPSPSVSPGYGHSVFQPGRLPLL LMGSPSPDPHSPSPQSSSKM*PLDLCVPFSPSVSPGYGHSVFQPGRLPLL IPTHSFLPGSVSGLLPPIRQYPMPWDSGGSGIPAFHLFFHLFVLFTLCTKK GLVYHRLLFLNRN   |
| 11  | 1              | 1     | A 74  | 651  | PFPQKK\PPKGIAPEEGSPFFF-NGS/PULEEPPKTFTLEKGSLQSFPGRI<br>EGGPRRLPP+RCPPRPAPWKRAPQ/GPLPLEEPPKTFTLEKGSLQSFPGRI<br>SSWAGREELCTRHHP+DLLSSRPPCPGPQMNPEAVLEPDG<br>SSWAGREELCTRHHP+DLLSSRPPCPGPQMNPEAVLEDCPLWPSERPLI  |
| 1   | 2              | +     | A 1   | 392  | GTRALCAGACHAHLLEMIANE*THLDPESKGR*V*INIMO**  \UNCTAFHDNEETFLTKYLYSLARTHSYYAPELLFFAKRDPSAFTECCQ/ D*AGCLLPKLDELRYEGKASSAIQRLK   |

|       |   | 511 |     | AFQKVADMATNTRGGTREIGSALTRMCMRHRSIEAKLRQFSSALIDCLINPL QEQMEEWKKVANQLDKDHAKEYKKARQEIKKKSSDTLKLQKKAKKGRGDIQP QLDSALQDVNDKYLLLEETEKQAVRKALIEERGRFCTFISMLRPVIEEEISM LGEITHLQTISEDLKSLTHDDPHKLPSSSEQVILDLKGSDYSWSYQTPPSSPS USSIDGGTISQDAFQSKSPSPMPPEAPNQRKEKREPDPNGGPTTASGPPA AAEEAQRPRSM AAEEAQRPRSM AAGEGQFKYVSWSSGPSGPGCTQRRSWKSTRGHSSLLPPSQDFVAGLSVIL AGRGGPGKFVSWSSGPSGPGCTQRRSWKSTRGHSSLLPPSQDFVAGLSVIL |
|-------|---|-----|-----|---|
| 10410 | A | 511 | 958 | AGRGGPGKPVSWSSGPGSPGQTQRRSWVKSTRGHSSLLFFGQD<br>RGTVDDRLNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTYPALREEAP<br>REHVESFFQKMDRNKDGVVTIEEFIESCQKDENIMRSMQLFDNVI  |
|       |   |     |     |   |

TABLE 9

|            |            |         | SEQ ID NOS:  |
|------------|------------|---------|--|
| TISSUE     | RNA SOURCE | HYSEQ   |  |
| ORIGIN     |            | LIBRARY |  |
| 0112-      |            | NAME    | 244 2004   |
|            |            |         | 18-19 49 87-90 240 246 424 471 835 944 1004  |
| dult brain | GIBCO      | AB3001  | 18-19 49 87-90 240 246 424 471 000 1000 1000 1000 1000 1000 1000   |
| duro       |            | 1       | 1021 1062-1063 1066 1092 1461 1<br>2227 2260 2277 2326 2583 2669 2942 2960 3107 2227 2260 2277 2326 2583 2669 2942 2960 3363                       |
|            | 1          | 1       | 2227 2260 2277 2326 2583 2669 3242 3244 3250 3363 3142 3176 3193 3196-3201 3242-3244 3250 3363 3142 3176 3193 3196-3201 3439 3490 3505 3530        |
|            | 1          | 1       | 3142 3176 3193 3196-3201 3242 3430 3505 3530 3398 3403 3420 3428 3431 3439 3490 3505 3530 3398 3403 3420 365                                       |
|            |            |         | 3398 3403 3420 3428 3431 3435 3436<br>3571 3753 3814 3822 3854 3956 3994 4020 4065   |
|            |            | 1       | 3571 3753 3814 3822 3854 3936 3936 4238<br>4101 4115 4159 4167 4196 4228-4229 4236 4238<br>4101 4115 4159 4167 4196 4238 4356 4380 4382            |
|            | 1          | 1       | 4101 4115 4159 4167 4196 4238 4356 4380 4382<br>4246 4259 4263 4267 4296 4338 4356 4380 4382   |
|            |            | 1       | 4246 4259 4263 4267 4296 4338 4359 4599 4407 4470 4494 4502 4521 4529 4549 4599 4705 4744 4769-4770  |
|            | 1          | 1       | 4407 4470 4494 4502 4521 4525 4541 4769-4770 4647 4653 4661 4679 4681 4705 4744 4769-4770 4647 4653 4661 4679 4681 4703 4913 4913 4928 4993        |
|            |            | l l     | 4647 4653 4661 4679 4681 4703 4713 4928 4993<br>4805 4867 4869 4900 4902-4903 4913 4928 4993   |
|            | 1          | 1       | 4805 4867 4869 4900 4902-4906 5261 5268 5301 5331 5073 5154 5208 5245 5249 5249 5408 5478 5505   |
|            | 1          | 1       | 5073 5154 5208 5245 5249 5201 5200 5408 5478 5505 5347 5351-5358 5363 5375 5399 5408 5478 5505 5701-5702 5705 5714                                 |
|            |            | 1       | 5347 5351-5358 5363 5375 5355 5405 5714<br>5572 5621 5640 5664 5685 5701-5702 5705 5714<br>5572 5621 5640 5664 5685 5701-5702 5705 5714            |
|            |            |         | 5572 5621 5640 5664 5685 5761 5789 5805 5859 5731 5736 5741 5757-5758 5763 5789 5805 6116  |
|            | 1          | 1       | 5731 5736 5741 5757-5738 5763 5763 6103 6116<br>5951 5992 6007 6037 6056 6061 6078 6103 6116<br>5951 5992 6007 6037 6056 6061 6078 6183 6187 6195- |
|            | 1          | 1       | 5951 5992 6007 6037 6056 6067 6183 6187 6195-<br>6119 6147 6156-6157 6159 6171 6183 6187 6195-   |
|            | 1          | 1       | 6119 6147 6156-6157 6159 6171 6160<br>6196 6200 6203 6215-6216 6221-6222 6224 6226<br>6196 6200 6203 6215-6216 6227-6224 6297 6344                 |
|            | 1          | 1       | 6196 6200 6203 6215-6216 6221-6224<br>6234 6239 6245 6248 6269 6287 6294 6297 6344<br>6234 6239 6245 6248 6269 6394 6419 6425 6455                 |
|            |            | 1       | 6234 6239 6245 6248 6259 6257 6257 6455 6356 6362-6363 6378 6380 6394 6419 6425 6455   |
|            |            | l l     | 6356 6362-6363 6378 6380 6357 6559 6562 6585 6457 6467 6534 6538 6540 6557 6559 6562 6585  |
|            | 1          | 1       | 6457 6467 6534 6538 6540 6537 6567 6616 6628 6590 6593 6595 6601-6604 6609-6610 6616 6628 6590 6593 6587 6687 6687 6687 6687                       |
| 1          | 1          |         | 6590 6593 6595 6601-6604 6609 6713 6718<br>6630 6635 6646 6659 6663 6687 6690 6713 6718  |
| 1          | 1          | 1       | 6630 6635 6646 6659 6663 6867 6050 6770 6776 6732 6734 6739 6752 6756-6757 6765 6770 6776  |
| 1          | 1          | 1       | 6732 6734 6739 6752 6758-6757<br>6785 6810 6842 6844 6854 6868 6880 6888 6895  |
| 1          | 1          | 1       | 6785 6810 6842 6844 6854 6856 6957 6960 7008<br>6900 6909 6918 6921 6932 6956-6957 6960 7008   |
| 1          | ł          | 1       | 6900 6909 6918 6921 6932 6936 7078 7089 7092 7030 7034 7041 7045 7064 7073 7088 7089 7092  |
| 1          | 1          | 1       | 7030 7034 7041 7045 7064 7073 7030 7034 7041 7057 7057 7057 7057 7057 7057 7057 705  |
| 1          | l          | l l     | 7111 7125 7136 7163 7163 7172 7472 7539 7575 7310 7335 7365 7379 7405 7454 7472 7539 7637 7639   |
| 1          |            | -       | 7310 7335 7365 7379 7405 7405 7630 7637 7639 7590 7599 7605 7608 7613 7618 7630 7674 7678 7692   |
|            | 1          | 1       | 7590 7599 7605 7608 7613 7613 7614 7678 7692 7642 7644 7646-7647 7649 7654 7674 7673 7731 7736 7738  |
| 1          |            | 1       | 7642 7644 7646-7647 7649 7654 7771 7736 7738 7699 7711 7719 7721 7726-7727 7731 7776-7778  |
| 1          | 1          | 1       | 7699 7711 7719 7721 7726 7770 7773 7776-7778 7745 7747 7750-7751 7766 7770 7773 7782 7829 7832   |
| 1          |            | 1       | 7745 7747 7750-7751 7766 7770 77818 7826 7829 7832 7789 7795 7802-7805 7807 7818 7826 7829 7832 7789 77924-7925 7943-7944                          |
| 1          |            | 1       | 7789 7795 7802-7805 7807 7818 7824<br>7864 7878 7884 7896 7915 7924-7925 7943-7944<br>7864 7878 7884 7896 7915 7924-7925 8018 8022                 |
| 1          | 1          | 1       | 7864 7878 7884 7896 7915 7924 7928 7878 7867 8000 8007 8009 8012 8018 8022 7948 7967 8000 8004 8007 8009 8013 8133 8139 8164                       |
| 1          |            |         | 7948 7967 8000 8004 8007 8003 8133 8139 8164<br>8045 8064 8093 8103 8113 8123 8133 8139 8164   |
| l l        |            | 1       | 8045 8064 8093 8103 8111 8123 8125 8167 8172 8174 8181 8186 8188 8201 8213 8215-   |
|            |            | 1       | 8167 8172 8174 8181 8186 8186 8261 8273 8281<br>8216 8219 8224 8233 8241 8259 8261 8273 8281   |
|            |            | 1       | 8216 8219 8224 8233 8241 8255 8269 8380 8405 8289-8290 8293-8294 8302 8305 8369 8380 8405 8289-8290 8293-8294 8451 8461 8510 8525                  |
|            |            |         | 8289-8290 8293-8294 8302 8303 8353 8553 8553 8553 8553 8553 8553   |
| 1          | 1          | 1       | 8408 8411 8427 8434 8448 8431 8431 8567 8616<br>8528 8545 8547 8560 8565 8580 8584 8587 8616   |
| 1          | 1          | 1       | 8528 8545 8547 8560 8565 8560 8561 8561 8561 8561 8561 8561 8643 8671 8683 8777 8795 8815 8820 8848 8857 8643 8671 8683 8797 8793 8930 8967 8988   |
| 1          | 1          | 1       | 8643 8671 8683 8777 8795 8615 8615 8615 8615 8615 8615 8615 861  |
| 1          |            | 1       | 8870 8881 8885 8893-8894 8923 8924 9226 9260 9420 9431 9077 9142 9188 9201 9224 9226 9260 9420 9431 9745 9811                                      |
| 1          |            | 1       | 9077 9142 9188 9201 9224 9226 38745 9811<br>9505 9546 9568 9599 9665 9733-9734 9745 9811   |
| 1          |            | 1       | 9505 9546 9568 9599 9865 9753 10349 10344 9866 9875 9952 10021 10260 10272 10384 10392   |
| 1          | 1          | 1       | 10350 10352 10356 10358 10307 10007  |
|            | 1          | 1       | 10398 10404 10407  |
| 1          | 1          | i i     |  |

TABLE 9

|        |          |        | 9537 9554-9555 9834 9838 9902 9941 9952 10003 10104 10125 10133 10167 10235 10339-10340 10348 10358 134 316 456-464 597-598 663 992 1092 1176 1327 134 316 456-464 597-598 663 992 1092 1176 2237-2238 2235  |
|--------|----------|--------|--|
| iterus | Clontech | UTROOL | 134 316 456-484 397-391 032-35-2236-2236-2251 1501 1576 1638-1640 1705 2277 2235-2236-2251 1501 1576 1638-1640 1705 2277 2235-2236-2251 12382-22383 2582 2779 2799 3043 3136 3190 3198 3323 2339 3420 3548 3726 3758 3793 3822 3848 3994 4139-4140 4202 4206 4300 4311 4329 4345 4360 4388 4405 4409-4410 4470 4497 4497 4504 4520 4555 4601 4661 4672 4674 4681 4723 4784 4858 4857 4903 4928 4953-4954 4956 4994 5031 5073 5155 5207-5208 5244 5421 5430 5445 5539 5544 5505-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 5605-5606 5614 5675 5685 5732 5741 5768 5784 6586 7690 6610 6632 6634 6641 6454 6459 6551 6553 6559 6599 6604 6616 6622-6623 6630 6659 6687 6709 6714 6727 6739 6765 6769 6777 6791 6794-6797 6816 6819 6842 6850 6865 6909 6930 6948 6958 7002 7013 7035 7084 7127 7134 7327 7546 6758 7002 7013 7035 7084 7127 7134 7327 7546 6758 7602 7764 7778 7780 7781 7818 7822 7884 7943 77948 7953 7974 7978 7980 7998 8004 8007 8019 8045 8064 8099 8133-8136 8163 8165 8172 8190 8045 8064 8099 8133-8136 8163 8165 8172 8190 8045 8064 8099 8133-8136 8163 8165 8172 8190 8197 8214 8228 8268 8273 8318 8338 8342 8346 8358 8387 8411-8412 8427 8435 8451 8461 8534 8358 8387 8411-8412 8427 8435 8451 8461 8534 8358 8387 8411-8412 8427 8435 8451 8461 8534 8564 8572 8580 8608 8616 8640 8654 8660 8752 8772-8773 8118 8839 8844 8853 8855 8866 8857 8772-8773 8118 8839 8844 8853 8855 8866 8857 8772-8773 818 8839 8848 8853 8855 8866 8857 8774 6950 9521 9596 9665 9710 9931 9903 10127 10131 10167 10344 10358 10375 10407 |

Table 10: Nearest neighbor (FastA v. Genbank, Genpept release 114)

|           | Tabl             | e 10: Nearest neighbor (FastA v. Genbank, Genpept Teleaso | SMITH-   | 8        |  |
|-----------|------------------|---|----------|----------|--|
|           |                  | DESCRIPTION   | WATERMAN | IDENTITY |  |
| SEQ<br>ID | ACCESSION<br>NO. |   | SCORE    |          |  |
| NO.       |                  |   | 1.50     | 34.043   |  |

| .  |      |                   |  | =-        | 34.043 |
|----|------|-------------------|--|-----------|--------|
|    |      |                   | Blastochloris viridis light harvesting complex   | 70        | 33.00  |
|    | M552 | 261               | Blastochloris Viriuis 11310  |           | 36,190 |
|    |      |                   | alpha-subunit  Homo sapiens alpha-1 type 2 collagen (714 AA)   | 99        | 38.710 |
|    | X13  | 783               | Homo sapiens alpha-1 type 2 collagen (712.2)  Gaenorhabditis elegans predicted using Genefinder;  Caenorhabditis elegans predicted using Genefinder;   | 140       | 30     |
|    | Z81  | 503               | Caenorhabditis elegans predicted using Comes similar to collagen; CDNA EST EMBL:D65450 comes similar to collagen; CDNA EST EMBL:D68888 comes from  |           | 1 1    |
|    |      | 1                 | similar to collagen; cDNA EST EMBL:D65500<br>from this gene; cDNA EST EMBL:D68888 comes from   |           | 1 1    |
|    | 1    | 1                 | from this gene; CDNA EST 2   |           | 37,333 |
|    | 1    | 1                 |  | 95        | 23.944 |
|    | 1138 | 3184              | this gene Trypanosoma cruzi ATPase subunit 6 Trypanosoma cruzi ATPase subunit 6  | 108       | 35,366 |
|    |      | 000323            | Trypanosoma cruzi Arrest<br>Escherichia coli putative ligase   | 256       | 76.154 |
|    |      | 022537            |  | 585       | 30.612 |
|    |      | 9974              | Warms caniens mariner transport  | 114       |        |
| !  |      | 038599            | Sus scrofa env protein   | 116       | 46.341 |
|    | AF   | 010886            |  | 198       | 30.000 |
|    | AB   | 010888            | Arabidopsis thaliana T8K14.10  Arabidopsis thaliana Teknarich proteoglycan   | 233       | 35.673 |
| LO |      |                   |  | 512       | 68.254 |
| 11 |      | 7318              | Rattus norvegicus profiles<br>Homo sapiens serum albumin precursor   | 144       | 46.535 |
| 12 | AF   | 190168            |  | 301       | 55.172 |
| 13 |      | 010144            | Drosophila melanogaster mus308   | 377       | 52.830 |
| 14 |      | 76559             | Canis familiaris ORF2  | 291       | 51.064 |
| 15 |      | 3012223           |  | 147       | 48.077 |
| 16 | X    | 03725             |  | 391       | 70.000 |
| 17 | Y:   | 12713             | Mus musculus elongation factor Tu  | 237       | 47.778 |
| 18 | M:   | 22432             | Mus musculus elongueles  | 396       | 33.514 |
| 19 | A    | F032103           | Homo sapiens ataxin-7  |           | 42.105 |
| 20 | U    | 51723             | Plasmodium vivax V-SERA 4  | 756       | 31.818 |
| 21 | A    | B023203           | Homo sapiens KIAA0986 protein  | 34        | 73.846 |
| 22 |      | F029676           |  | 292       | 38.136 |
| 23 |      | 164983            | Homo sapiens fibrinogen beca   | 241       | 41.975 |
| 24 |      | 413101            | Rattus norvegicus unknown protein  | ) 180     | 46.575 |
|    | -1;  | AB02348           | - antiva Similar to Zeu may  | 202       |        |
| 25 |      | X53581            | Destuc norvegicus ORF4   | 247       | 49.412 |
| 26 |      | AB01222           | Canis familiaris ORFZ  | 275       | 50.000 |
| 27 |      |                   |  | 359       | 60.000 |
| 28 | _    | X52235            | Homo sapiens ORFII  Mus musculus Pro-Pol-dUTPase polyprotein  Mus musculus Pro-Pol-dutPase polyprotein   | 497       | 40.343 |
| 29 | _    | Y12713<br>AC00302 |  |           |        |
| 30 | 1    | AC00302           | line found   | 173       | 39.583 |
| _  | _    |                   | line found Rattus norvegicus coding sequence of pol  | 439       | 66.038 |
| 31 |      | V01201            | Rattus norvegicus coding sequence Organical Residence Organica Residence Organica Residence Organica Residence Organica Reside | r: 180    | 27.381 |
| 32 |      | X17025            |  | ,         |        |
| 33 | 3    | AL1172            | preliminary prediction   | 397       | 82.558 |
| L  |      |                   | Homo sapiens titin   | 530       | 70.73  |
| 34 | 4    | X69490            |  | 187       | 35.78  |
| 3  | 5    | AB0004            |  | 483       | 68.06  |
| 3  | 6    | M13100            | Rattus norvegicus dansem 110 } 48 Homo sapiens KIAA0648 protein  |           | 50.00  |
| 3  |      | AB0145            | 48 Homo sapiens KIAA0648 protein Mus musculus phosphatidylinositol 3-kinase 110 b  | Da 331    | 30.00  |
| _  | 8    | U03279            | Mus musculus phosphacidyiinos  |           | 72.72  |
| 13 | -    |                   | subunit contract coxidase assembly protection  | ein   171 | /2.72  |
| 1  | 9    | AF0443            | subunit 21 Homo sapiens cytochrome c oxidase assembly prote  |           | 72.22  |
| 3  |      | 13.0.4            | COX11 Homo sapiens paraneoplastic cerebellar   | 391       | 12.22  |
| L_ | 10   | D1298             | Homo sapiens paraneoplastic celeboria  |           |        |

|       |          | imprinted gene, Peg3.  | 921     | 40.921 |
|-------|----------|--|---------|--------|
|       | L35604   |  | 1483    | 97.357 |
|       |          | Pattus norvegicus GIP-Dinding pat  | 9350    | 99.927 |
| .055  | U54807   |  | 289     | 32.609 |
| 1000  | AB002359 | Homo sapiens KIAA0361<br>Unknown cDNA EST yk448c11.3 comes from this   | 203     | 1      |
| 10396 | Z81564   | Unknown cDNA EST yk448C11.3 comes from this gene; gene; cDNA EST EMBL:C09223 comes from this gene;   |         |        |
|       |          |  | 737     | 32.083 |
|       | AL109630 |  | 1405    | 92.511 |
| 10397 |          | Drosophila melanogaster Enterprise Prosophila melanogaster Prosophila mela | 1       |        |
| 10398 | D10376   |  | 2092    | 99.694 |
|       |          | isozyme 3 synthetic construct vascular anticoagulating   |         |        |
| 10399 | A01771   | protein brotein  | 137     | 26.316 |
|       |          | Schizosaccharomyces pombe hypothetical p   | 325     | 49.438 |
| 10400 | Z99162   | Homo sapiens Unknown   |         | 87.372 |
| 10401 | AF131851 | Homo sapiens Unknown Homo sapiens guanylate binding protein isoform I  | 1215    | 99.471 |
| 10402 | M55542   |  | 751     | 50,917 |
| 10403 |          | Rattus norvegicus statumin und und und und und und und und und un  | /31     |        |
| 10404 | AL021106 |  | 1       | 1      |
|       |          | ( method: "denscan , vo  | 115     | 23.61  |
|       |          |  | 175     | 26.27  |
| 10405 |          | to differ applicus hypothetical process  | 2274    | 68.11  |
| 10406 |          |  | 217     | 34.61  |
| 10407 | Z48334   |  | 226     | 23.89  |
| 10408 | AC006955 | Arabidopsis thaliana unknown plees<br>Homo sapiens Fas-ligand associated factor 3  | 589     | 78.70  |
| 10409 |          |  | 1 2 6 9 |        |
| 10410 | AF120102 | Homo sapiens carsenization   |         |        |

|          |     |          |             | AMINO ACID SEQUENCE ENCODED BY THE NUCLEOTIDE  |
|----------|-----|----------|-------------|--|
|          | Me- | Predict- | Predict-    | AMINO ACID SEQUENCE ENCORES ENCORE SEQ ID NO. SEQUENCE OF THE CORRESPONDING SEQ ID NO.   |
| SQ.      |     | ed beg-  | ed end      | SEQUENCE OF THE CORRESPONDENCE  (A=Alanine, C=Cysteine, D=Aspartic Acid,  (A=Alanine, C=Cysteine, D=Aspartic Acid,  (A=Alanine, C=Cysteine, D=Aspartic Acid,   |
| 0        | th- | inning   | nucleo-     | (A=Alanine, C=Cysteine, D=Asparts  E= Glutamic Acid, F=Phenylalanine, G=Glycine,  E= Glutamic Acid, F=Phenylalanine, G=Glycine,  |
| ο.       | od  |          | tide        |  |
|          | 1   | nucleo-  | location    | H=Histidine, 1=1801edcino, N. Acparagine,  |
|          | 1   | tide     | corres-     | H=Histidine, I=Isoleuthe, N=Asparagine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, P=Proline, Q=Glutamine, N=Tryptophan,   |
|          | 1.  | location | ponding     |  |
|          | 1   | corres-  | to last     |  |
|          | 1   | ponding  |             | T=Threonine, V=Valinow, *=Stop Codon,<br>Y=Tyrosine, X=Unknown, *=Stop Codon,<br>Y=Tyrosine, X=Unknown, *=Stop Codon,  |
|          | 1   | to first | amino       | / micleotide deletion, . 1   |
|          |     | amino    | acid        | nucleotide insertion)  |
|          | 1   | acid     | residue     | nucreocras   |
|          | 1   | residue  | of amino    | 1  |
|          |     | of amino | acid        |  |
|          | 1   | acid     | sequence    |  |
|          | 1   | sequence |             | AIFKCVEGMFRIAMVNVCFVSSGSLLI*PLTY/GYYDEWTHFAYM  |
|          | +   | 114      | 436         | AIFKCVEGMFRIAMVNVCFVSSGSEED WISPNTGSFAYPVYPKSL   |
| 1        | A   | 114      |             | AIFKCVEGMFRIAMVNVCFVSSGSLLL*FLIT/<br>TIDLLEIPITGSHPVVLNALFCLEAP\WISPNTGSFAYPVYPKSL   |
|          | 1   | 1        |             | IAHDFAVEATMPYIRLSSI  |
|          |     |          | 467         | KSNIPNLGDCGWESLFNR\QSWKSSLAV\RDTTOOTHER\AN HADLCTLSDKDRPITIQTALAELVKHKPKATYEQLIAVLDEF/AN   |
| 2        | A   | 124      | 467         |  |
|          |     | l .      | 1           | FLKKWWKAYDKENLFCEEG*KLCAASN  |
|          | - 1 | 1        |             | FLKKWWKAYDKENLFCEEG*KLCAASN  SKQMITIHNTKGRT*SLILVSLIIFIATTNLLGLLPYSFTPTTQL  SKQMITIHNTKGRT*SLILVSLIFIATTNLLGLLPYSFTPTTQL   |
| 3        | A   | 2        | 453         | SKQMITIHNTKGRT*SLTLVSLIIFIATINDGUSH<br>SINLAMAIPL*AGAEVICLQFFFN/NSLAS*/MPKVRITMIIVML<br>SINLAMAIPL*AGAEVICLQFFN/NSLAS*/MPKVRVYYKCVR  |
| ,        | 1   | 1        | 1           | SINLAMAIPL*AGAEVICLQFFFN/NSLAS*/TUSTON SINLAMAIPL*AGAEVICLQFFN/NSLAS*/TUSTON SINLAMAIPL*AGAEVICLQFTN/NSLAS*/TUSTON SINLAMAIPL*AGAEVICLQF |
|          | 1   | 1        | 1           | CSIPSTRGYPFLVRSDL  |
|          | 1   | 1        | 1           | CSIPSTRGYPFLVRSDL<br>EGFLELLRTRNHSNSQLQLTTGIGLFLNEGLKLVDKFLEDV*K*Y<br>EGFLELLRTRNHSNSQLQLTTGIGKIVDLVKELDRDTVFD   |
|          | - A | 1        | 427         | EGFLELLRTRNHSNSQLQLTTGGLFENGESING<br>HSETFTVNFSDTE*AMKHINDYVEKGTQGKIVDLVKELDRDTVFD<br>HSETFTVNFSDTE*AMKHINDYSTVNEPIMKLLS\ML  |
| 4        | A   | 1 *      | 1           | HSETFTVNFSDTE*AMKHINDYVEKGIQGKIVDE<br>LANYIFFKGKWDRPFEVNDTEEEDFHVDQVSTVNEPIMKLLS\ML  |
|          | 1   | 1        | 1           | LANYIFFKGKWDRPFEVNDIEEEDE  |
| l        | 1   | 1        | 1           | NIHPCFKL<br>KIKSFYASKDTIKRMRVTDWKKIFAY*ISDKELIFTLRTLKT**K  |
|          |     |          | 465         | KIKSFYASKDTIKRMRVTDWKKIFAY*ISDKDWSTSLVSELAPCE<br>*GKQPNLKNGQEI*VPISPQDIQIAHK\HLEGWSTSLVSELAPCE   |
| 5        | A   | 1        | 1.00        | *GKQPNLKNGQEI*VPISPQDIQIAHK\nlick*<br>APV/RHPLTGLTIAGLQGFGEAGRLVRGRWGC*W/VHPF*KYI/W  |
| l        | 1   | 1        | 1           | APV/RHPLTGLT1AGLQGFGEAGRE  |
| 1        | - 1 | 1        | 1           | QFLSKLHISLPYDPTTPLLGTCSR QFLSKLHISLPYDPTTPLLGTCSR  |
| 1        | L_  |          |             | QFLSKLHISLPYDPTTPLLGTCSK HFVIHSKHDLAIAHLGIY/PREMKT*VHTKTCT*IFTVALSVIAR   |
| 6        | A   | 308      | 3           | HFVIHSKHDLAIAHLGIY/PREMKI*VHIKACI AWNQPGRPLCSEWL\KYMVHTME*HSAIKRLNYRYKNNCVNLFLG  |
| 1        | 1   | 1        | 1           | ITLSEKSQTQNVI  |
| 1        | - 1 |          |             | ITLSEKSQTQNVI  FLTRETGDPTGRSSSHANTQSRFFPDDPPG\PLNNLGNTHGCGRR FLTRETGDPTGRSSSHANTQSRFFPDDPPG\PLNNLGNTHGCGRR   |
| 7        | A   | 587      | 2           | FLTRETGDPTGRSSSHANTQSRFFPDDPFQ'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGRSSSHANTGSRFFPDDPG'\{ FLTRETGDPTGTGSRFFPDDPG'\{ FLTRETGDPTGTGSRFFPDDPG'\{ FLTRETGDPTGTGSRFFPDDPG'\{ FLTRETGDPTGTGSRFFPDDPG'\{ FLTRETGDPTGTGSRFFPDDPG'\{ FLTRETGDPTGTGSRFFPDDPG'\{ FLTRETGDPTGTGSSHANTGSTGSTGSTGSTGSTGSTGSTGSTGSTGSTGSTGSTGST  |
| 1'       | 1   | 1        | 1           | AGRCPGTGPDGP\AGCGGPRCWPSGHLAATO EAGPAGFTACSPLSGCRTPYTHHFPASRMSCHLNCASPRTYRSQG EAGPAGFTACSPLSGCRTPYTHHFPASRMSCHLNCASPRTYRSQG  |
| 1        | - 1 | 1        | 1           | EAGPAGFTACSPLSGCRTPYTHHFPASKMSCHIMCOPAKCRKPRNRR<br>NRGCERVAQGSQGAGGERGAKSQVPVPAPARNKDPAKCRKPRNRR   |
| 1        | - 1 | ł        | 1           | NRGCERVAQGOQGAGG   |
| 1        | - 1 | 1        |             | PGNSGPVVRAYRRQR<br>RILNEEHGKYEGLHE*EVKWHLYIKSPAFTDLHLCYQKDMNGIST   |
| <u> </u> |     |          | 475         | RILNEEHGKYEGLHE*EVKWHLYIKSPATIDLE*LTIFKTESR<br>SASSPAVGTVGMDMDEDDDFSKWNFYYSPHSYPDK*LTIFKTESR<br>SASSPAVGTVGMDMDEDDDFSKWNFYYSPHSYPDK*LTIFKTESR  |
| 8        | 7   | ٠ ١٠     |             | SASSPAVGTVGMDMDEDDDFSKWNF115FIB1120<br>VRESDEVTQIKVNWDEEVISGLLTSLKDNVLKATGVLYDYAYK\Y   |
| 1        | 1   | 1        | 1           | VRESDEVTQIKVNWDEEVISGEEISE   |
| 1        | - 1 | 1        | 1           | LCEHTRSTLKEESLKLERNLONN  |
| 1        |     |          | 539         | LCEHTRSTLKEESLKLERNLQNH SQCSPFISPACSLTALEEETEALRVHPRLCLSPNLAPSSGPPRPI  |
| 9        |     | A 3      | 1539        | SQCSPFISPACSLTALEEETEALKVHPKRCHSFKTYTCI<br>ELAPCPPSSQAGLRTCHSWVKGLHQPLPVASGMKSTFCNKTYTCI<br>ELAPCPPSSQAGLRTCHSWVKGLHQPLPVASGMKSTFCNKTYTCI  |
| 1-       | 1   |          | 1           | ELAPCPPSSQAGLRTCHSWVKGLHQPLPVASGTH*<br>YPPP/PPLCPNHSPNALTLPDSVTHAVPFE/L*SPSAPPSSTA*<br>YPPP/PPLCPNHSPNALTLPDSVTHAVPCPCAPRAWQRDGT   |
| 1        | 1   | 1        | 1           | YPPP/PPLCPNHSPNALTLPDSVITAVFFELZ LGSPS\CGASPCNHPHSHPGICPTPPGLWPVCPCAPRAWQRDGTH   |
| 1        | 1   | 1        | 1           | Treats (count count  |
| ł        | - 1 | 1        |             | QT RL*LGLEYALLVWGTPKV*H*GGFPIYYYIVLLLSYALHQVTEY  |
| L-       |     | A 2      | 453         | RL*LGLEYALLVWGTPKV*H*GGFPITTTTNLIGNWPSTVSLWLV. MYVSIMAFNAKVSDPLIVGTYMTLLNTVSNLIGNWPSTVSLWLV.   |
| 10       | 1   | A 2      | 1           | MYVSIMAFNAKVSDPLIVGIIIII CKKI GGSCVTALDGYYVESII  |
| - 1      | 1   | 1        | 1           | PLTVKECV*TSYQNCCTPDAAEECIGGGGGGG   |
| 1        | 1   | ı        | 1           | VSIAFV/W*VFLVHKFK  |
| 1        | ١   |          | <del></del> |  |
| 11       |     | A 20     | 475         | KMGVPPLLMSDPNRFLFPKNFLKEKTISFFK<br>LNFLGFPGFKIFFPVFKFFFFFFFF/RDRVSLYHPGWSAVSQSE  |
|          |     | 1        |             |  |

TABLE 11

|       | A              | 1   | 140  | KTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFIN<br>KQADAYVBKGILDKERAEAIKRIYSSL<br>NTSVAIQTIEYYSAFKRKETLTHVPLWMNLKDTMLREISQSQKDT   |
|-------|----------------|-----|------|---|
| 14069 | A              | 1   |      | V<br>QNAKVGSEAIQVLPAFPREVQRLPEPAKSCRQRQLEARKAAAEKK  |
| 14070 | A              | 3   | 1654 | KIQKEKLSTPEKIKQEALELAGITSIN OF SDPYSMISVYSYKSYY VEPOMIFSSFKYSGANVESYSVLGNCR PSDPYSMISVYSYKSYY AQPSLTSVNGPHSKYALPSFSYYGFBSSNYPPSQFLGPDANGHS GSSGFEKKPDLHALINKLSPAYGABFAELBSQAVPTDAHHPTP HQQPAYPGFKEYLLPKAPLLHSVSRDPSPFAQSSNCYNRSIKQE PVDPLTQAEPVFRDAGKMGKTPLSEVSQNGGPSHLMGYSGGPSH SPKRTNGYGGSMOVPSSGESPAIVPDKLSSFGASCLAPSHFTDGQ WGLFPGESQQAASHSGGRLBGKMSFCKFGNSTSLALPSHFTDG WALGGDPNSALKGSPGFOKLMNPKKEEBGRIPAAGASQLVFYQ HKNILQPNHGLALMEAMKGLAERARAAQEEAARLGLQQEAKLY GKKRKNGGTVVAEPQQKEKGVVPTRQALAPPTBSATVSSYAYT KVTGPYSEMI |
| 14071 | 1 <sub>A</sub> | 212 | 104  |   |
| 14072 |                | 358 | 112  | FPLTVMLNVFLWWQNLKHFCHT2FU<br>GLELLGSTNLPASVSRVAGTTGIHNCTQFNPLHTLHL<br>YMGFHHVGYAGLELLTSSDLPPWPPKCWDYRHEPSCLAMFFYFAL   |
| 14073 | A              | 3   | 151  | IAPE TARREST CIVE PVPRIDLTNIDQVA  |
| 1407  | 4 A            | 8   | 1493 | VTIHHLFYGQAVRADTLKKRSSCHLOKT VIFKHHFYGGRÖAVLKTMAPAQCLCSRMGPAWLHLLGTG ILAGV HCQPLLAHGDKSLQGPQPERHQLSEPAPAYHRIFPTITNFALRLY KKLAADAPON IFFSFVSISTTLALLSLGAQANTSALLLEGLGFRL TTFDRADIHQGFRSLLHTLALDSPKLELKVGNSLFLDKRLKPROH YLDSIKELYGAFAFSANFTDSVTTGRQINDYLRRQTYGQVVDCLE EFSQDTFMVLANYIFFKAKKHIFPSRYQTKQGSFFVDERTSLQV PMMHKKRHHFLYDQDLACTVLQIEYRGNALALLVLDDFGKNKQV EAALQPOTLEKMGQLLPSLLDLHLDRFSISGTYMLEDILDPGIG TNILMLEADFSGYTGQLNKTISKVSHKAMYDMSEKGTEAGAASGI LSQPSLNTHSDPHAHFNRFFLLLLMEVTTQSLLFLGKVVNFVA                      |

TABLE 12

|             |            |                  | SEQ ID NOS:   |
|-------------|------------|------------------|---|
| TISSUE      | RNA SOURCE | HYSEQ<br>LIBRARY |   |
| ORIGIN      |            | NAME             | 220 240 1011 1155   |
|             |            | AB3001           | 88 550 603-604 606-613 622 848 1011 1155  |
| adult brain | GIBCO      | ABSOUL           | 88 550 603-604 606-813 622 625<br>1354 1501 1988 2153 2156 2158 2176 2281<br>1354 1501 1988 2153 2895 2899 3022 3121-   |
|             | 1          | ١                | 1354 1501 1988 2153 2156 2159<br>2362 2380 2528 2586 2895 2899 3022 3121-   |
|             | 1          |                  | 3123 3127-3128 3132-3133 3260 3657 3712   |
|             | 1          | 1                | 3295 3305 3307 3379 3440 300 4045-4046  |
|             | 1          | 1                | 3732 3820 3833 3862 3922 4301 4322 4417   |
| }           |            |                  | 4049 4067 4218 4225 4277 4334<br>4428 4439 4698 4702 4753 4778-4779 4781<br>4428 4439 4698 4702 4977 5074 5112 5130   |
|             |            | 1                | 4428 4439 4698 4702 4733 4776<br>4786 4798 4879 4899 4977 5074 5112 5130<br>4786 4798 4879 5307 5520 5564 5596  |
|             | 1          | 1                | 4786 4798 4879 4899 4977 5520 5564 5596<br>5155 5201 5209-5210 5307 5520 5564 5596  |
| 1           | 1          | 1                | 5155 5201 5209-5210 5307 5328 6025 6104<br>5699 5725 5768 5944 5952 5989 6025 6104<br>5699 5725 5768 5944 5952 6390 6423 6428   |
| 1           | 1          | 1                | 5699 5725 5768 5944 5932 300 6423 6428<br>6223-6226 6229 6268 6361 6390 6423 6428<br>6223-6226 6229 7316 7328 7515 7552-  |
| 1           | 1          | 1                | 6223-6226 6229 6268 6351 6350 5350 5350 5350 5350 5350 5350 5350  |
| 1           | 1          | l .              | 6847 6949-6952 7037 7118 7221<br>7553 7555-7559 7561 7564 7637 7646 7821<br>7553 7555-7559 8125 8145 8170 8180  |
| 1           | 1          | 1                | 7553 7555-7559 7561 7564 7637 18180 7852 7924 7930 8095 8125 8145 8170 8180 7852 7924 7930 8095 8125 8145 8170 8180   |
| 1           | 1          | 1                | 7852 7924 7930 8095 8125 8125 8127 8200 8284 8286 8358 8433 8488 8513 8517 8200 8284 8286 8358 8358 8358 8488 8513 8517   |
|             |            | 1                | 8200 8284 8286 8358 8433 8433 8483 8584 8584 8597 8710 8734 8736-8741 8743-8746 8880 8597 8710 8734 8736 8739 9108 9146 9195  |
| 1           | 1          | 1                | 8597 8710 8734 8736-8741 8736 9146 9195<br>8902-8903 8935 8964 9079 9108 9146 9195<br>8902-8903 8935 8964 9079 9572 9586 9637   |
| 1           | 1          | 1                | 8902-8903 8935 8964 9079 9100 3210<br>9326 9333 9373 9386 9529 9572 9586 9637<br>9326 9333 9373 9386 9529 971 10002 10037 10073   |
| 1           | 1          | 1                | 9694 9807 9854 9865 9671 10763 10865  |
| 1           | 1          | 1                | 10373 10407 10550-10551 1000-   |
| 1           | 1          | 1                | 10874 10985 11077-11073 11201 11923 11970   |
| 1           | 1          | 1                | 11225 11240 11336 11367 12147 12241   |
| 1           | 1          | 1                | 11978-11984 11986-11989 12123 12543 12557<br>12274 12410 12480 12492 12523 12543 12557<br>12274 12410 12480 12493 12739-12740 12743   |
| 1           | 1          | 1                | 12274 12410 12480 12492 12523 1253<br>12586 12659 12690 12713 12739-12740 12743<br>12586 12659 12690 12713 12739-12740 12743  |
| ١           | 1          | 1                | 12586 12659 12690 12713 12877 12959 13048<br>12811 12814 12840 12867 12877 12959 13048  |
| 1           | 1          | l l              | 12811 12814 12840 12867 12877 12323<br>13052 13085-13087 13141 13204 13213 13223  |
| 1           | 1          | 1                | 13052 13085-13087 13141 13222 13399 13534<br>13282 13291 13294 13305-13307 13399 13534  |
| l l         | 1          | 1                | 13282 13291 13294 13305-13307 13642 13648 13600 13624 13635 13637 13640 13642 13648   |
|             |            | 1                | 13600 13624 13635 13637 13640 13752<br>13650 13652 13655 13715 13752-13753 13785  |
| 1           | 1          | 1                | 13650 13652 13655 13715 13732 13836<br>13796 13802 13805 13816 13836 13842 13886  |
| 1           | 1          | 1                | 13796 13802 13805 13816 13836 |
| 1           |            |                  | 13949 13962 14029 14034 14057<br>72 88 147 449 593 604 614-615 617 619-630  |
| adult bra   | in GIBCO   | ABD003           | 72 88 147 449 593 604 614 615<br>639 737 740 743 -748 766 806 -807 816 1155<br>639 737 740 743 -748 766 806 -807 816 1155   |
|             | 1          | 1                | 639 737 740 743-748 766 85 85 85 85 85 85 85 85 85 85 85 85 85  |
| 1           | 1          | 1                | 1159 1174-1192 1201 1354 1415<br>1583 1679 1767 1785 1844 1988 2153 2160<br>1583 1679 222 2281 2315-2317 2319-2322<br>2191-2193 2252 2281 2315-2317 2319-2322   |
| 1           | 1          | 1                | 2191-2193 2252 2281 2313 2528 2533 2572<br>2360 2380 2429 2461 2466 2528 2533 2572<br>2360 2380 2429 2461 2468 2528 2930 2945   |
| 1           | 1          |                  | 2360 2380 2429 2461 2466 2326 2930 2945<br>2586 2593 2631 2734 2828 2895 2930 2945<br>2586 2593 2631 2734 3143 3146 3148 3150-  |
| 1           |            | 1                | 2586 2593 2631 2734 2625 2655 3148 3150-<br>3022 3115 3136 3141 3143-3146 3148 3150-<br>3022 3115 3136 3141 3143-3146 3288-3290   |
| 1           | l l        | 1                | 3022 3115 3136 3141 3143 3143 3143 3143 3143 3143   |
| 1           | l          | 1                | 3152 3256 3276-3278 3260-3263 3307 3309 3293-3297 3299-3300 3303-3304 3307 3309 3293-3297 3292-3307 3560 3571   |
| l l         |            | 1                | 3293-3297 3299-3300 3303 3507 3560 3571<br>3371 3379 3401 3458 3482 3507 3560 3571  |
| 1           | l          | l                | 3371 3379 3401 3458 3482 3507<br>3618 3628 3648 3650 3657 3709-3720 3723<br>3618 3628 3648 3650 3657 3709-3780 3820   |
| 1           | 1          | 1                | 3618 3628 3648 3650 3657 3760 3780 3820<br>3725 3732 3734 3743 3745 3760 3780 3820  |
| Į.          | 1          | 1                | 3725 3732 3734 3743 3743 4049 4064<br>3827 3833 3862 3879 4030 4043 4049 4064   |
| 1           | 1          | 1                | 3827 3833 3862 3879 4030 4045<br>4079 4081-4082 4084 4102 4218 4225 4270<br>4079 4081-4082 4084 4104 4461 4650  |
| 1           | 1          | 1                | 4079 4081-4082 4084 4102 4213<br>4277 4301 4307 4419 4434 4441 4461 4650<br>4277 4301 4307 4419 4434 4441 4461 4650   |
| 1           | 1          | 1                | 4277 4301 4307 4419 4434 4431<br>4652 4671 4685 4720 4782 4795 4822 4841<br>4652 4671 4685 4720 4782 4894 4894 4896   |
| 1           | 1          | 1                | 4652 4671 4685 4720 4782-4782<br>4871 4879 4881-4883 4886-4892 4894-4896<br>4871 4879 4881-4887 4894 4999 5009 5035   |
| 1           |            | 1                | 4871 4879 4881-4883 4880-4891<br>4898-4903 4939 4977 4994 4999 5009 5035<br>4898-4903 4939 4977 4997 5113 5130 5145   |
| 1           | 1          | l                | 4898-4903 4939 4977 4934 5058 5068 5074-5075 5077 5113 5130 5145  |
|             |            |                  |   |

TABLE 12

|        |          |        | 12557 12559-12560 12734 12742 12862-12863 12954-12955 13033 13038-13039 13052 13059 13102 13105 13110 13114 13127 13168-13169 13448-13450 13515-13516 13640 13832 13879 13889 13942-13948 13970 14054 13970 14054 141 1254-1258 1332 1501 1503-1519 1043 1141 1254-1258 1332 1501 1503-1519   |
|--------|----------|--------|---|
| uterus | Clontech | UTRO01 | 1043 1141 1241 1254 1250 2381 2326 2343 2360 1630 1679 1940 2160 2281 2326 2343 2360 1630 1679 1940 2160 2281 2326 2343 2360 2384 2409-2414 2572 3304 3502 3743 3780-3783 3785 3993-4010 4112-4114 4216 4225 4270 4301 4419-4420 4464 4545 5035 5039 5222 5339-5340 5520 5532-5545 5699 5739 5756 5840 5987 6169 6529 6633-6641 6649 6925 7060 7101-7102 7371 7544 7955-7959 8106-8115 8117-8119 8121 8170 8206-8207 8212 8286 8322 8402 8684 8739 9075 9159 9204 9321-9326 9403 9439 9483 9535 9608 9774 10098-10099 10203-10209 10425 10679 10744-10752 10790-10792 11240 11336 11387 11475 11477-11484 11797 11936 12484-12486 12488-12491 12561-12562 12690 12796 12820 12956-12958 13029 13049 13061 13141 13186 13199 13213 13223-13224 13271 13402 13419 13451-13453 13517-13519 13537 13655 13655 13663 13879 13949 13951-13954 14034 14037 |

TABLE 13

| 270 | N.C.C  | ESSION    | DESCRIPTION  | SMITH-<br>WATERMAN | % ID | ENTITY |
|-----|--------|-----------|--|--------------------|------|--------|
| EQ  |        | MBER .    |  | SCORE              |      |        |
| ID  | IN.    |           | 1 1 140  | 222                |      | 55     |
| 10: | M36    | 501 H     | omo sapiens alpha-2-macroglobulin  | 332                |      | 64.423 |
|     | A00    | 270       | unthetic construct Human Serum   | 319                | _    | 64.583 |
|     |        |           |  | 714                |      | 80.282 |
|     | V00    |           |  | 213                |      | 36,196 |
|     | 4 X01  |           | norwegicus unknown protein   | 163                |      | 42.391 |
|     | 5 M13  |           | Homo sapiens unknown protein   | 163                |      | 30.682 |
|     | 6 M22  |           |  | 74:                |      | 80.392 |
|     |        |           | Mytilus edulis precorragem<br>Homo sapiens apolipoprotein B fragment   |                    |      | 30.872 |
|     | 8 X03  |           |  | 17                 |      | 85.43  |
|     | 9 ABO  | 19280     | Mus musculus sprouty-* Homo sapiens acetyl-coenzyme A transporter  | 81                 |      | 0.0    |
| 1   | 0 D88  | 3152      | Homo sapiens acecyl-coencyms   | 16                 | -    | 35.443 |
| 1   | 1 X9   | 2485      | Plasmodium vivax pval  | 28                 | 9    | 80.597 |
|     |        |           | Homo sapiens KIAA0445 protein  | 16                 | 6    | 33.01  |
|     | 3 L3   | 5013      | Homo sapiens spliceosomal protein  | 37                 | 4    | 55.085 |
|     | 14 L2  |           |  | 63                 | 8    | 74.15  |
|     | 15 U4  | 9973      |  | 1                  |      |        |
| -   | 15 04  | 3313      |  | 24                 | 18   | 40.625 |
|     | 16 110 | 9116      | Trama caniens ORFZ, encoues a 20   |                    |      |        |
|     | 1000   | 7110      | transcriptase homolog  | 1                  | 52   | 37.778 |
| -   | 17 AF  | 010144    | transcriptase homolog<br>Homo sapiens neuronal thread protein AD7c-  |                    |      |        |
|     |        |           |  |                    | 41   | 36.364 |
|     | 18 X   | 53581     | Rattus norvegicus ORF4   | 7                  | 37   | 80     |
|     |        | F183961   | Homo sapiens carbon catabolite logical   |                    |      |        |
| 1   | 17     |           | 4 protein homolog  | 7                  | 67   | 85.417 |
| -   | 20 A   | J002190   | 4 protein homolog<br>Homo sapiens dihydroxyacetone phosphate   |                    |      |        |
|     | -      |           | acyltransferase  | 2                  | 25   | 48.22  |
| -   | 21 Y   | 12713     | Mus musculus Pro-Pol-dolfase political vk452h4.3   | 2                  | 11   | 32.33  |
| -   |        | 74026     | Mus musculus Pro-Poi-uoireae poor<br>Caenorhabditis elegans cDNA EST yk452h4.3<br>comes from this gene; cDNA EST yk452h4.5 | 1                  |      |        |
| 1   |        |           | comes from this gene, course   |                    |      | 66.89  |
| 1   |        |           | comes from this gene Homo sapiens ORF1; MER37; putative  |                    | 521  | 66.89  |
| -   | 23 (   | 149973    | Homo sapiens ORFI; MERSY, pater<br>transposase similar to pogo element   |                    | _    | 72.3   |
| 1   | _      |           | Homo sapiens neuronal thread protein AD7c  | -                  | 198  | 12.3   |
|     | 24     | AF010144  | Homo sapiens neuronal chief  |                    |      | 50.39  |
|     | - 1    |           | NTP Homo sapiens ATPaseII  |                    | 321  | 86.39  |
|     |        | AB013452  |  | r                  | 782  | 86.33  |
|     | 26     | D38595    |  |                    |      | 61.47  |
|     |        |           |  |                    | 389  | 37.70  |
|     |        | U49974    |  | 1                  | 177  | 37.7   |
|     | 28     | Z92803    | Unknown predicted using General School EST similar to GTP-binding protein; cDNA EST  | 1                  | 1    |        |
| 1   |        |           |  |                    | 167  | 34.9   |
| -   |        |           | Mus musculus guanna nucleotide   |                    | 16/  | 54.5   |
|     | 29     | L07924    | Mus musculus guanine<br>dissociation stimulator  |                    | 150  | 61.7   |
| L   |        |           |  |                    | 279  | 30.6   |
|     |        | U79260    |  |                    | 279  | 30.6   |
| Г   | 31     | U76604    | antigen 2/type XVII collagen   |                    | 287  | 41.0   |
| L   |        |           |  |                    |      |        |
|     |        | AB01222   |  |                    | 606  |        |
| Г   | 33     | X03145    |  | n                  | 140  |        |
|     | 34     | AC00623   |  |                    | 233  |        |
| _   | 3      | 5 AF00353 | - Warne ganiens ORFZ-like process  |                    | 672  | 83.    |
| · - |        | 6 M15386  | Homo sapiens gamma-globin  |                    |      |        |

TABLE 13

|       |          | comes from this gene; c  | 122  | 69.565 |
|-------|----------|--|------|--------|
| 24067 | AF107406 | Homo sapiens GW128   | 2980 | 99.145 |
|       |          | Homo sapiens secretogranin III   | 139  | 48.718 |
|       | U62039   | Elephantulus edwardii reverse  |      |        |
| 14069 | 062039   | transcriptase  | 2399 | 100    |
| 14070 | AB007861 | Table No. N. T. A. O. A. O. A. C. A. | 69   |        |
|       | X07816   | Human herpesvirus 4 epitope Cl3 (57 AA)  | 128  | 45.455 |
|       | S58722   | Human herpesvirus & cpreep   |      |        |
| 140,2 |          | (C-terminal, clone XEH.8C)   | 136  |        |
| 14073 | AB006136 | Homo saniens FUT1  | 1128 | 43.972 |
|       | L19684   | Homo sapiens kallistatin   |      |        |
|       |          |  |      |        |

TABLE 14

|      |     |          |          | AMINO ACID SEQUENCE ENCODED BY THE NUCLEOTIDE  |
|------|-----|----------|----------|--|
| , T  | Me- | Predict- | Predict- |  |
| Q    | th- | ed beg-  | ed end   | SEQUENCE OF THE CORRESPONDENCE Acid, (A=Alanine, C=Cysteine, D=Aspartic Acid, (A=Alanine, C=Cysteine, D=Aspartic Acid,   |
|      |     | inning   | nucleo-  | (A=Alanine, C=Cystelne, D=Asparent<br>E= Glutamic Acid, F=Phenylalanine, G=Glycine,<br>E= Glutamic Acid, F=Phenylalanine, G=Glycine,   |
| ٠. ا | od  | nucleo-  | tide     | E= Glutamic Acid, F=FHenylardine,  |
|      | l   |          | location | H=Histidine, I=Isoleucine, N=27  |
|      | 1   | tide     | corres-  | H=Histidine, I=Isoleucine, N=Asparagine,<br>L=Leucine, M=Methionine, N=Arginine, S=Serine,   |
|      |     | location | ponding  |  |
|      | 1   | corres-  | to last  |  |
|      |     | ponding  |          | T=Threonine, V=Valine, W=Tr-Tr-Tr-Tr-Tr-Tr-Tr-Tr-Tr-Tr-Tr-Tr-Tr-T  |
|      |     | to first | amino    | /-nossible nucleotide deletion, (1   |
|      | 1   | amino    | acid     | nucleotide insertion)  |
|      | 1   | acid     | residue  | nucleocido   |
|      | 1   | residue  | of amino |  |
|      | 1   | of amino | acid     |  |
|      | 1   | acid     | sequence |  |
|      |     | sequence |          | LKGVNSPIKKPRVASFFKKNPRPLVFCF*K/T/HLFCKCPPGVQKK   |
|      |     | 2        | 199      | LKGVNSPIKKPRVASFFKKNPRFLUTTO   |
| L    | A   | 12       |          | LKGVNSPIKKPRVAGTTUREN STATELING STAT |
|      |     |          | 2321     | GWGKIFPANWKPKKTGGGLINFUKIAF**** FKKNFFPPRVWGFFSPFSP*KSSSPPKAFIFLGGVGPIFPPPKKRF FFKNSQGGVFPF/PPVFKNRPRPCFFLPPPPSSSSSSP\PPVNFGP  |
| 2    | A   | 1        | 2321     | PRINCOGGUEDE/PPVFKNKPRPCFFHF1120000  |
|      | 1   | 1        |          | PRVFFKGPPPSSSSSSSSLRQS   |
|      | 1   |          |          | PRVFFKGPPPSSSSSSSSSSLRQS YAKLGTRILRLVKNPPAATGGCPPASEAQASSQFALSSALYLPGEG YAKLGTRILRLVKNPPAATGGCPPASEAQASSQFALSSALYLPGEG   |
| 3    | A   | 2        | 517      | YAKLGTRILRLVKNPPAATGGCPPASEAGASUZ<br>\QSMVPVEKMRSAGSRG*WRRAA*QPWCSGSRAPPWPPWAASATTS  |
| -    | 1   | 1        |          |  |
|      | 1   |          |          | SSATA\LPQLSDGH-1/SVF1TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  |
|      | 1   |          |          | APGQLPGTSLVPLGGSQPSQPCPLFHSTM: KWAGTGAGAPDPLQSGLVTTPTQPGFRPTL/PAPPCSGLPCPRAPP KWAGTGAGAPDPLQSGLVTTPTQPGFRPTL/PAPPCSGLVLGPVPTCFCPQP   |
| 4    | A   | 471      | 911      | KWAGTGAGAPDPLQSGLVTTPTQPGFRFTD/<br>WYTPSQGAGDPPPRTQAADAQEHRARPCPPSAGVLGPVPTCFCPQP<br>WYTPSQGAGDPPPRTQAADAQEHRARPCPPSAGVLGPVPTAGS   |
| 4    | \^  |          | 1        | WYTPSQGAGDPPPRTQAADAQEHRARFCFFGAG<br>ALSP*LHPWPT*KVPSHALQPAKALAHLTLHGQHCPHASHVP*AGS  |
|      | 1   |          |          | ALSP*LHPWPT*KVPShALQFAIGLE   |
|      | 1   |          |          | HCSCCEFPDT ARTFPLALDEAAGRGAAAEGPAALLG\PAGFRWAEPGAALGRGLAA ARTFPLALDEAAGRGAAAEGPAALLG\PAGFRWAEPGAALGRGLAQ   |
|      |     | 1        | 1250     | ARTFPLALDEAAGRGAAAEGPAALLG YAGYKING<br>VVGRGATWRRGRCPAGRIVPSVPARCALLPPSGAAGQGQRGQLRQ<br>VVGRGATWRRGRCPAGRIVPSVPARCALLPPSGAPGGSAFCSPPAA   |
| 5    | A   | 1        | 1220     | VVGRGATWRRGRCPAGRIVPSVPARCADDFFORMAG<br>RRR*AGRALQPGSGQLRPCPA/PPGVRRPQPRGAPGQSAFCSPPAA<br>RRR*AGRALQPGSGQLRPCPA/PPGVRRPQPRGAPGQSAFCSPPAA   |
|      | - 1 | 1        | l l      | RRR*AGRALQPGSGQLRPCPA/PPGVRRPQFRGATCE  |
|      |     | 1        |          | RRR*AGRALQPGSGQLRPCPA/PPGVRRFQFRGRLSLPSSVYPS<br>LDKLRALCGSATPKARPGEAAQRVGSDLGSSGPRGRLSLPSSVYPS<br>LDKLRALCGSATPKARPGEAAQRVGSDLGSSGPRGRLSLPSSVYPS   |
|      |     |          | ì        | LDKLRALCGSATPKARPGEAAQRVGSDBSSGK TOTALLEQAAP WSVP\PGPSGVPGVPGGADCS/P*QEGRGQGTDDPEVPALNEQAAP WSVP\PGPSGVPGVPGGADCS/PKESASGLDISTPQHSSG*SD  |
|      |     | 1        |          | WSVP\PGPSGVPGVPGGADCS/P*QEGRGG1UDISTPQHSSG*SD<br>TSWQASFWDRGDIAGKCSGGSRGLRKESASSGLDISTPQHSSG*SD<br>TSWQASFWDRGDIAGKCSGGSRGLRKESASSGLDISTPQHSGASTVAP/GSGNQSPPTMCGA  |
| 1    |     | 1        |          | TSWQASFWDRGDIAGKCSGGSRGLKALSASSUM<br>P*LAPGHL*GSQAAGDRWPGRPLLPGAGTVAP/GSGNQSPPTMCGA<br>P*LAPGHL*GSQAAGDRWPGRPLLPGAGTVAP/GSGNQSPPTMCGA  |
| 1    | - 1 | 1        | 1        | P*LAPGHL*GSQAAGDRWPGRPLLPGAGTVAT/<br>PGD*VANGKPPCFSGARAAS\GSEETPLPSAPHLSLGDTRAPYPGQ<br>PGD*VANGKPPCFSGARAAS\GSEETPLPSAPHLSLGDTRAPYPGQ  |
| l    | - 1 | 1        | 1        | PGD*VANGKPPCFSGARAAS\GSEE1PLFSARMOSE<br>*WRGISTGVLGLHLLPSLHVFPAPPSARARPPGRSFPASGLCPPAS   |
|      |     | 1        | 1        | *WRGISIGVEGENEESE CENT   |
| 1    |     | 1        |          | RRPGNSGQ<br>SIVWTATLFLLEQKGTLKMTDQTSTSQMMTQKVNLLKRAKERQIS*   |
| -    | A   | 31       | 319      | SIVWTATLFLLEQKGTLKWIDQISISQMITQK<br>GR*RECK\IQRPCRKSVNKMLFVLVLEFAICWAPFHIDRLFFSFVE   |
| 6    | A   | 1 32     |          | GR*RECK\IQRPCKKSVMKHHI VZVZZ   |
| 1    | - 1 |          | 1        | EWSE  GGEPYRRNEDKPVA\ACGAIANSVFNDTLKKVLIGFDW*PIPMGWK   |
| L    |     |          | 421      | GGEPYRRNEDKPVA\ACGATANSVFNDTERCTCVPGNWLKPAYMLDSE   |
| 7    | A   | 125      | 72.      | GGEPYRRNEDKPVA\ACGATANSVFNDT LIKKV<br>KNGIAWRTDKRVKFKNPPGGDNLGERFKGTSVPGNWLKPAYMLDSE   |
| 1    | - 1 | 1        | 1        | PNNNGFI  |
|      |     |          |          | PNNNGFI  FFLRWSL/DSVAPAKVQWRDLGSGQAPGFTPFSCLSLPSSWDYRHE FFLRWSL/DSVAPAKVQWRDLGSGQAPGFTPFSCLSLPSSWDYRHE   |
| 8    | A   | 2        | 319      | FFLRWSL/DSVAPAKVQWRDLGSGQAPGF1FF000<br>PPRPANFFVFSVEMGF\TMLARMISIS*H\VDPPTSVSQNAGITGN  |
| ١    | 1   | 1        | 1        | SHRASLDILLLNVLLS   |
|      | - 1 | 1        |          |  |
| 9    | A   | 1        | 729      | LAVKMALSRVCWARTAVLGSAVIFGHFVIRTLGVVIFPRFLY\L<br>SKLHLSPKADVKNLMSYVVTKTKAINGKYHRFLGVVIFPRFLY\L<br>SKLHLSPKADVKNLMSYVVTKTKAINGKYHRFLGVVIFPRFLY\L   |
| ١٩   | I A | 1-       | 1        | SKLHLSPKADVKNLMSYVVTKTRAINGKTHAT<br>TIFMKGRIADVMG\DAKKG*RNKAQLCEGQL*GFINFQSREMEHLI<br>TIFMKGRIADVMG\DAKKG*RNKAQLCEGQL*GFINFQSREMEHLI   |
|      | - 1 | 1        | 1        | TIFMKGRIADVMG\DAKKG*RNKAQUCEGGU QFRQDVPKCLFIGIISIPPFANYLVFLLMYLFPRQLLIRHFWTPK QFRQDVPKCLFIGIISIPPFANYLVFLLMYLFPRQLLIRHFWTDLCTK   |
| - 1  | 1   |          |          | QFRQDVPKCLFIGIISIPPFANYLVFLIGHTELFRQUERWRLTDLCTK   |
| -    |     | 1        |          | OTDFLDIYHAFRKQSHPEIISILEKVII BISSI   |
| - 1  | 1   | 1        | 1        | QRGTHPACMRPLR VIETECNLVEPLIDI*SK   |
| - 1  | - 1 |          |          |  |
| 1    | 0 1 | 1        | 283      | KSVYCW*\NIQLIKPFWKAVWHSLVALNITI<br>CSCVPGARIKIFTALLFILTLIT/VNKNLEHL*HPAEVEWVNQFW   |
| -    |     |          | 1        | IYIY   |
|      |     | 1        | ı        | 1 1111   |

TABLE 14

|      |   |      | 366  | ESTILISTLPPAIEMTSTAPPSTPTAPTTTSGHTLSPPSSTTTSP PGTPTRGTTTGSSAPTPSTVQTTTTSAMTPTFTLSTPSITRTTG LRPYPSSVLICCVLADTYAPGEEVYNTYGDTCYFVNCSLSCTLE FYMWSCPSTPSPTPTPSKSTPTPSKPSSTSKFFGTKPPECPDFD PFRGENETWHLCDCFMATCKYNNTVELVKVECPPPPMFCSNGLOP VRVEDDEGCCHHWECDCCYCTGWGDPHYVTPDGLYSYGGNCTYVLV WREDSGCCHHWECDCCYCTGWGDPHYVTPDGLYSYGGNCTYVLV MIMPMQVQVANRQAVLFYKYGLEVYQSGINTVVDIPELGVLYSY MGLSFSVLPYHRGMNTKGQCGTCTNTTSDDCILFSGSIVSNCBA AADQMLVNDPSKPHCHSSSTTKRPAVTVDGGKKTPHKDCTPSFL CQLIKNSLPARCHALVPPQHYYDACVFDSCFMPGSSLECASLQAYA ALCA GULLITMNVLFSVVIFATFVTLCNASCYFIPRGVPGDSTRKMD |
|------|---|------|------|---|
| 5381 | A | 3    |      | LKGNKHPINSEWQTDNCETCTCYETEISCCIDGGT<br>IFKKEDCKYIVVEKKDPKKTCSVSEWII   |
| 6382 | A | 3    | 367  | LILHHKVYDLTKFLEMSKTFIIGELHFDDATIONAL<br>SSSWWTNWVIPAISAVAVALMYRLYMAED   |
| 6383 | A | 136  | 437  | LTPPTASPPPLPQLDPCPPGICPFPPPLFFWFTAGE LWARRKEL   |
| 6384 | A | 119  | 226  | HPFHCRPGWSTVVESQLTEASISTIQVED NLQPEAGTVSLADMQKHDCSRDDDDEKCFAFPTLPISQALCYHPLP  |
| 6385 | A | 1625 | 1862 | RTHTHTHTHTHTHTHTHTQSTCRISQRHTFRA  |
| 6386 | A | 394  | 473  |   |
| 6387 | A | 1177 | 1787 | EAFGSGRPHTGFEPSSPPAPVEAGAKKAVKSGVKSG<br>GFKPAHALPLTDQARGMAGNRPAQPCGGHGADCRPPTTLRAPRSQE<br>RVQGDTMQVAPTGLSLARTEFGTLPLLDAGVCGEAGGGMQTNRPPH<br>SERGTCPVTPPTPSDSPLI<br>SERGTCPVTPPTPSDSPLI  |
| 6388 | A | 643  | 754  | - POWNI CLEINMYTYGLALGVEERMRASVRGAGEWRCVIII   |
| 6389 | A | 76   | 304  | KDFPQRQRGFSAAAAPPCSSLPHFQPGRCC  |
| 6390 | A | 27   | 365  | PEGLHQEHPALSPAPUPQHPSHPAPUPFQT  |
| 6391 | A | 3    | 354  | RCRNSARAEPRITESCREAFRS FREE ROLL<br>LKEKRDMLDKEISQFVSEGYSVDELEDHITQLHEYNDIKDVGQML<br>GKLAVIRGVTTKELYPEFGLDMND   |

TABLE 15

| TISSUE ORIGIN  RNA SOURCE LIBRARY LIBRARY ABJOURD  adult brain  GIBCO  AB3001  2 4 17 77 140 433 508 828 952 1084 1125 1183 1446 1555 1615 1689 1788 1803 1865 1931 1945 2031 2056 2154 2453 2689 2724 2738 -2739 2772 2787 2920 2941 2967 3100 3177 3179 3227 3242 3321 3356 3360 3360 3361 3412 3424 3432 3446 3449 3453 349 3655 3749 3755 3789 3791 3889 3977 3982 398 4006 4180 4195 4198 4205 4251 4255 429 4216 4427 4429-4430 4556 4596 4600 460 4672-4673 4676 4722 4752 4759 4777 482 4685 4906 4939 5096 5110 5117 5130 515 5326 5342 5350-5351 5362 5365 5371 537 5385 5389 5392 5403 5425 5427 5457-545 5385 5389 5392 5403 5425 5427 5457-545 5385 5389 5392 5403 5425 5427 5457-545 5482 5501 5505-5506 5508 5511 5514-551 5485 551 5505-5506 5508 5511 5514-551 | 4<br>5 3160 |
|---|-------------|
| ORIGIN   LIBRARY   NAME   2 4 17 77 140 433 508 828 952 1084 1125   183 1446 1555 1615 1699 1788 1803 1865   183 1446 1555 1615 1699 1788 1803 1865   183 1846 1855 1615 1699 1788 1803 1865   183 1846 1855 1615 1619 1788 1803 1865   193 1945 2031 2058 2154 2453 2689 2724 2738 2779 2772 2787 2920 2941 2967 3100 3177 3179 3227 3242 3321 3356 3360 3365 3412 3424 3432 3446 3449 3453 3492 3655 3749 3756 3789 3791 3889 3977 3982 398 4006 4180 4195 4198 4205 4251 4255 429 4416 4427 4429-4430 4556 4596 4600 460 460 46072-4673 4676 4722 4752 4759 4777 482 4885 4906 4939 5096 5110 5117 5130 515 5152 5365 5371 537 5326 5342 5350 5351 5362 5365 5371 537  | 4<br>5 3160 |
| Adult brain GIBCO AB3001 2 4 17 77 140 433 508 828 952 1084 1122 1183 1446 1555 1615 1689 1788 1803 1865 1931 1945 2031 2058 2154 2453 2689 2724 2738 2739 2772 2787 2920 2941 2967 3107 3177 3179 3227 3242 3321 3356 3360 336 3361 3412 3424 3432 3446 3449 3453 3492 365 3412 3424 3432 3446 3449 3453 3492 365 3474 3756 3789 3791 3889 3977 3982 3983 3749 3756 3789 3791 3889 3977 3982 3984 4006 4180 4195 4198 4205 4251 4255 429 4416 4427 4429 4430 4556 4596 4600 460 460 4672 4673 4676 4722 4752 4759 4777 482 4858 4906 4939 5096 5110 5117 5130 515 5326 5342 5350 5351 5362 5365 5371 537 5326 5342 5350 5351 5362 5365 5371 537  | 4<br>5 3160 |
| 1183 1446 1555 1615 1699 17/88 1608 2724 1931 1945 2031 2058 2154 2453 2689 2724 2738-2739 2772 2787 2920 2941 2967 3107 3177 3179 3227 3242 3321 3356 3360 336 3412 3424 3432 3446 3449 3453 3492 365 3749 3756 3789 3791 3889 3977 3982 398 4006 4180 4195 4198 4205 4251 4255 429 4416 4427 4429-4430 4556 4596 4600 460 4672-4673 4676 4722 4752 4759 4777 482 4885 4906 4939 5096 5110 5117 5130 515 5326 5342 5350-5351 5362 5365 5371 537 5326 5342 5350-5351 5362 5365 5371 537   | 4<br>5 3160 |
| 1931 1945 2031 2058 2194 2493 205 273 100 2738 2739 2772 2787 2920 2941 2957 3100 3177 3179 3227 3242 3321 3356 3360 3361 3412 3442 3432 3446 3449 3453 3492 365 3749 3756 3789 3791 3889 3977 3982 398 4006 4180 4195 4198 4205 4251 4255 429 4206 4180 4195 4198 4205 4251 4255 429 4216 4427 4429 4430 4556 4596 4600 460 46072 4673 4676 4722 4752 4759 4777 482 4885 4906 4939 5096 5110 5117 5130 515 5326 5342 3350 5351 5362 5365 5371 537 5326 5342 3350 5351 5362 5365 5371 537   | 6 3160      |
| 2738-2739 2772 2787 2920 2941 2937 2942 2937 2943 2937 2943 2937 2942 2943 2936 336 336; 3412 3424 3432 3446 3449 3453 3492 365; 3412 3424 3432 3446 3449 3453 3492 365; 3749 3756 3789 3791 3889 3977 3982 398 4006 4180 4195 4195 4205 4251 4255 429 4416 4427 4429-4430 4556 4596 4600 460 4672-4673 4676 4722 4752 4759 4777 482 4885 4906 4939 5096 5110 5117 5130 515 5326 5342 5350-5551 5362 5365 5371 537 5326 5342 5350-5551 5362 5365 5371 537   |             |
| 3177 3179 3227 3242 3321 3330 3300 3300 3300 3300 3300 330  |             |
| 3412 3424 3432 3446 3449 3433 3432 3848 3477 3982 398 3749 3756 3789 3791 3889 3977 3982 398 4006 4180 4195 4198 4205 4251 4255 429 4416 4427 4429-4430 4556 4596 4600 4672-4673 4676 4722 4752 4759 4777 482 4885 4906 4939 5096 5110 5117 5130 515 5326 5342 5350 5351 5362 5365 5371 537 5326 5365 5371 537  |             |
| 3749 3756 3789 3791 3889 3977 3882 4825 429 4006 4180 4195 4198 4205 4251 4255 429 4416 4427 4429-4430 4556 4596 4600 460 4672-4673 4676 4722 4752 4759 4777 482 4885 4906 4939 5096 5110 5117 5130 515 5326 5342 5350-5351 5362 5365 5371 537  |             |
| 4006 4180 4195 4198 4203 4231 4231 4231 4231 4231 4231 4231 423   |             |
| 4416 4427 4429-4430 4556 4595 4707 482<br>4672-4673 4676 4722 4752 4759 4777 482<br>4885 4906 4939 5096 5110 5117 5130 515<br>4885 4906 4939 5096 5110 5117 5130 515<br>5326 5342 5350-5351 5362 5365 5371 537  |             |
| 4672-4673 4676 4722 4/52 4/52 4/53<br>4885 4906 4939 5096 5110 5117 5130 515<br>5326 5342 5350-5351 5362 5365 5371 537<br>5326 5342 5350-5351 5362 5365 5371 537  |             |
| 4885 4906 4939 5096 5110 5117 517 5371 5371 5371 5372 5365 5362 5365 5371 537   |             |
| 5326 5342 5350-5351 5362 5363 5372 54   | 4 5321      |
|   |             |
| 1 5385 5369 5372 547  |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
| 5710-5711 5713 5718 5720 5721 5703 5767 5782 57<br>5734 5738 5749 5751 5763 5767 5782 57  | 89 5/95     |
|   |             |
|   |             |
| 5910 5913 5931 5946 5964 6022 6255 62<br>6141-6142 6146-6147 6154 6222 6255 62  | 92 6290     |
|   |             |
|   | 12 020      |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
| 2080 2121 2453 2465 2702 2724 2733 2<br>2595 2621 2637 2689 2720 2724 2733 2<br>2746-2747 2753 2763 2764 2764 2767 2  | 845 2901    |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
| 3950 3965 3986 3989 3991 4000<br>4017 4041 4043 4048 4082 4112 4167 4   | 4188 4195   |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
|   |             |
| 5250 5256 5259 5263 5273 5210 5541<br>5325 5327 5330-5331 5336-5337 5341  | 5542 5541   |
|   |             |

TABLE 15

|   | 3889 3982 4112 4182 4238 4244 4297 4376 4421   |
|---|--|
|   | 3889 3982 4112 4182 4236 4777 4891 4906 4963<br>4459 4505-4506 4559 4596 4777 4891 4906 4963 |
| 1 | 4459 4505-4506 4559 4596 4777 1000 5369 5387 5403  |
| 1 | 4459 4505-4506 4555 4556 5368 5387 5403<br>5076 5110 5123 5273 5313 5350 5368 5387 5403      |
| 1 |  |
| 1 |  |
| 1 |  |
| 1 | 5695 5701 5704-5705 5710 5717<br>5747-5748 5758 5761-5763 5767 5782 5789 5793                |
| 1 | 5747-5748 5758 5761-5763 5767 5702 5935 593  |
|   |  |
| 1 | 5841 5854 5878 5864 5041 6118 6152 6183 621<br>5944 5946-5947 5949 6041 6118 6152 6183 621   |
|   | 6241 6255 6285 6302 6375 6380  |
| 1 | 6241 6255 6285 6302 6373 666   |
|   |  |

TABLE 16

|        |         |          | DESCRIPTION   | SMITH-   | *<br>IDENTIT | ~     |
|--------|---------|----------|---|----------|--------------|-------|
| EQ     |         | ESSION   | рдоска-   | WATERMAN | IDENTIT      | 1     |
| ID     | N       | UMBER    |   | SCORE    |              | 44    |
| 10:    |         |          | Homo sapiens putative p150  | 156      |              |       |
|        | U93     |          | Homo sapiens putative particles Helianthus annuus hydroxyproline-rich | 169      | 36.3         | 64    |
| 2      | M76     |          |   |          | 34           | 94    |
|        |         |          | nombe WiskOtt-  | 163      | 34.          | -     |
| 3      | Z98     |          |   | 198      | 32.5         | 76    |
|        | -       |          |   | 270      |              |       |
|        | L21     |          | Canis familiaris type I collagen pre-                                 | 270      | 31           | 1.0.  |
| 5      | AF1     | 53062    |   | 180      | 36           | .17   |
|        | -       |          | pro-alpha1(I) chain Homo sapiens orphan G protein-coupled             | 180      | 1            |       |
| 6      | AF      | 44601    | receptor; GPC-R   | 175      | 44.          | 595   |
|        | -       |          | receptor; GPC-R<br>Caenorhabditis elegans No definition               | 1/-      | 1            |       |
|        | 7 06:   | 1953     |   | 32       | 67.          | 708   |
|        | +       | 000011   | line found Homo sapiens neuronal thread protein                       | 32.      | 1            |       |
| 1      | BAF     | 010144   |   | 18       | 5 25.        | 568   |
|        | 0 252   | 0018     | hila melanogaster ANON-66DD   | 14       |              | 333   |
|        |         |          | la thur porvegious unknown procesn                                    | 16       |              | 286   |
|        |         | 3100     |   |          |              | .667  |
|        |         | 4492     | Onchocerca volvulus pyrrolidone-rich                                  | 14       | 1 21         | .007  |
| 1      | 2 AF    | 055985   |   | 18       | 35           | .227  |
|        |         |          | antigen<br>Homo sapiens ORF1 codes for a 40 kDa                       | 1.       | 33           |       |
| 1      | 13 ME   | 30344    |   | 29       | 1 43         | .151  |
|        | _       |          | Tiomo capiens p64 myc protein   |          |              | .062  |
|        |         | 10493    | warma samiens p64 myc protein   |          |              | .294  |
|        |         | 10493    | iong unknown protein  |          | 71           | .872  |
|        |         | 22334    | Acanthamoeba castellanii myosin I                                     | 1        | 91 34        | .0/2  |
|        | 17 U    | 67056    |   |          | 10 20        | . 986 |
|        | $\perp$ |          |   | 2        | 42 28        |       |
|        | 18 M    | 80341    |   |          | 43 5:        | 1.685 |
|        | $\perp$ |          | Homo sapiens ORF2-like protein  | 1        |              | 2.53  |
|        |         | F003535  | Homo sapiens KIAA0187   |          | 13           | 8.636 |
|        |         | 80009    |   |          |              | 5.50  |
|        |         | 88460    | Mus musculus procollagen type V alpha                                 | 1        | .44 3        | 5.50  |
|        | 22 1    | 02918    |   |          |              | 1.75  |
| 1      |         |          | Homo sapiens transformation-related                                   | 1        | 288 5        | 1./5  |
|        | 23      | L24521   |   |          |              | 1.09  |
| L_     |         |          | protein Homo sapiens ORF2-like protein                                |          | 150          | 41.8  |
|        |         | AF003535 |   |          | 243          | 2.64  |
|        |         | AF003535 | Homo sapiens neuronal thread protein                                  |          | 157 4        | 2.64  |
|        | 26      | AF010144 |   |          |              | 19.20 |
|        |         |          | AD7c-NTP Homo sapiens ORF2-like protein                               |          |              |       |
|        |         | AF003535 |   |          | 177          | 19.31 |
|        |         | AF003535 |   |          | 20,1         | 56.16 |
|        |         | AB012223 |   |          | 182          | 38.4  |
| +      |         | AF118023 | Homo sapiens SH3 domain-binding                                       |          |              |       |
| -      |         |          |   |          | 132          | 30.5  |
| 1      | 31      | X77816   | Rattus norvegicus PR-Vbetal   |          | 255          | 52.6  |
| -      |         | X83413   | Human herpesvirus 6 U88   | _        | 221          | 52.0  |
| -      |         | X83413   |   | en       | 187          | 28.5  |
| -      |         | M88593   |   | C11      | 170          | 40.5  |
| <br> - |         | X05561   |   |          |              |       |
| - 1    | 35      | VOSSOT   | (AA -27 to 917) (2953 is 2nd base in                                  | 1        |              |       |

TABLE 16

|      |   | Y MPCP7  | 10912 | 100    |
|------|---|--|-------|--------|
| 369  | AB011540                                | Homo sapiens AMP-activated protein                   | 175   | 34.884 |
| 5370 | U22456                                  | Homo sapiens AMP-activated prosession                |       |        |
|      |   | kinase homolog Aquifex aeolicus hypothetical protein | 165   | 24     |
| 6371 | AE000762                                | Aquifex aeolicus hypotheticus F                      | 123   | 64.516 |
| 6372 | AF159055                                | Homo sapiens leucine zipper-like                     |       |        |
|      |   | protein Acropora donei mini-collagen                 | 127   | 33.333 |
| 6373 | D30747                                  | Acropora doner mini-corrage                          | 131   | 38     |
| 6374 | X52164                                  | Mus musculus Q300 protein (AA 1-77)                  | 4273  | 100    |
| 6375 | AB014516                                | Homo sapiens KIAA0616 protein                        | 130   | 31.579 |
| 6376 | A31036                                  | Nicotiana alata PRP2                                 | 351   | 93.103 |
|      | M12623                                  | Homo sapiens high mobility group                     |       |        |
| 05   |   |  | 75    | 36.113 |
| 6378 | D29833                                  | Homo sapiens proline rich peptide P-B                | 207   | 100    |
|      | 270292                                  | Homo sapiens chemokine CC-1                          | 9126  | 100    |
|      | M94131                                  | Warma capiens mucin                                  | 801   | 99.12  |
|      | M15885                                  | Homo sapiens seminal plasma protein                  | 002   |        |
| 6361 | 1115005                                 | progurgor  | 603   | 76.11  |
| 628  | 2 M22865                                | Homo sapiens cytochrome b5                           | 118   | 58.62  |
|      | 3 AF010427                              | Hepatitis E virus ORF-1; hypervariable               | 110   |        |
| 630. | AL OLOUE                                | magion   | 134   | 66.66  |
| 628  | 4 AJ131190                              | Homo sapiens FANCA protein                           | 160   | 57,89  |
|      | 5 579410                                | Mug sp nuclear localization signals                  | 100   |        |
| 030  | 5,5,5,5                                 |  | 113   | 8      |
| 638  | 6 AJ388513                              | (NLS)-Binding protein Space (NLS)-Binding protein L6 | 183   | 29.29  |
|      | 7 AF039052                              | Caenorhabditis elegans No definition                 |       |        |
| 050  | ,,                                      | line found   | 93    | 48.14  |
| 638  | 8 X67703                                | Drosophila melanogaster Mst84Dc                      | 112   | 41.66  |
|      | 9 AJ388550                              | Canis familiaris hypothetical protein                | 128   | 33.3   |
|      | 0 X01779                                | tradam inilgare C-hordein iragment                   | 117   | 26.0   |
|      | 91 AL109822                             | Schizosaccharomyces pombe hypothetical               | 11/   | 20     |
| 03:  | 7 | protein  | l     |        |

| SEQ<br>ID<br>NO | Method | Predicted<br>start<br>nucleotide<br>location<br>for amino<br>acid<br>sequence | stop<br>nucleotide<br>location | Amino acid sequence encoded by the nucleotide sequence of the corresponding SEQ ID NO.  (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Typotphan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=Possible nucleotide deletion,   \text{-Possible nucleotide insertion} |
|-----------------|--------|---|--------------------------------|--|
|                 |        |   |                                |  |

|            | 23    | 76 MN                          | NLILRRHLNKNYFCY  |
|------------|-------|--------------------------------|--|
| 1 C<br>2 B | 1     | 735 MS<br>GV<br>MV<br>ED<br>PQ | GDISONGMFLREEGIGN IRLT TARY VULT<br>TSCPSYNEKLVPDKKLKIRYTHSSDFGKSILCNTLTIIMDQLVKGGGAI<br>TSCPSYNEKLVPDKKLKIRYTHSSDFGKSILCNTLTIIMDQLVKGGGAI<br>TSCPSTRESSCHOMHTIRTSGFFRADPKISIYPDVDILMSNRQSS<br>KGLTQPCSGLSVCANDHTSCHOPKISCHOPKISCHOPKISCH<br>MLLIPTRRNLKPRIQAKNNDSQVPMKSWMDVELGNVLADSRGRCE<br>MLLIPTRRNLKPRIQAKNNDSQVPMKSWMDVELGNVLADSRGRCE<br>MSSRAGTSRERRSLPPIYGLQLLCPVIFGWPLPTGSTGRKSEDEKR  |
| 3 B        | 1     | RA<br>RH<br>NII<br>PL<br>G     | K SERRAGLPPSLPDRGRAGEHDGSSNSRGGAGRQARSIARRHSEAI PSERRAGLYDQRDLHANIPNSIVHANQNVHQPRMHEQQGNGHEKKL IGPTVMNLKNARPAASIELHHLFGVHNRTQRATRLQTPLPSPRAPT RGGAPYLVGSTLSHLGSGKRPEGGRGSSGGGSGVGSRPAERIDGA RGAPYLVGSTLSHLGSGKRPEGGRGSSGGLLSPARGFTGAPGP PRPPLPAFLNAFVFLDPGTQPRAPTGGNSSQGLLSPARGFTGAPGP TSFSATTTCQETPPQLPICPQMF   |
| 4 B        | 104   | 266 XI                         | IPYHTPWNPRQEKYDQRDLHANIPNSIVHANQNVHQPRMHEQQGNC<br>WKGTAETWAYMDEPQKR  |
| 5 B        | 1     | G<br>S<br>R<br>V<br>Y<br>T     | WKGTAETWAYMDEPQRK  IKRPNSDLSTNCSGTKVCLDPAYGEEDEGLPGRLPEGEGLREPTECD  IKRPNSDLSTNCSGTKVCLDPAYGEEDEGLPGRLPEGEGLREPTECD  IKRPNSDLSTNCSGTKVCLDPAYGEEDEGLPGRLPEGEGLREPTECD  IKRPSUNGSIAWSVLTGGSQEMRLQGKIAMANAECLCRARPCASAL  CPTAQQARHPDTILPROLGHWKAVTRVKLLNSYHGRSPFTTLRHSKT  KESIWNKQSIANQNALFGPTQVSLTAFITGLKRPCKSFSASTGCRFLI  KESIWNKQSIANQNALFGPTQVSLTAFITGLKRPCKSFSASTGCRFLI  KESIWNKQSIANQNALFGPTQVSLTAFITGLKRPCKSFSASTGCRFLI  KESIWSTAVQPETQDGQLRSFDTIWQLRAQRNSIISVNQRINSLQGLCI  TTGMVSAVQPETQDGQLRSFDTIWQLRAQRNSIISVNQRINSLQGLCI  TTGMVSAVQPETQDRDAGRSHSGSRSHKLRTEPASSQHKGRCSK  TYQKGINTDLKSTYPQKPDAGRSHSGSRSHKLRTEPASSQHKGRCSK  TYQKGINTDLKSTYPQKPDAGRSHSSSRSHKLRTEPASSQHKGRCSK  TYQKGINTDLKSTYPQKPDAGRSHSS  TYGKGAGNAGRSHSSANG  TYGKGTAGNAGRSHS  TYGKGTAGNAGRSHSSANG  TYGKGTAGNAGRSHSANG  TYGKGTAGNAGRSHSANG  TYGKGTAGNAGRSHSANG  TYGKGTAGNAGRSHSANG  TYGKGTAGNAGRSHSANG  TYGKGTAGNAGN |
| 6 C        | 3     | 164                            | MFRIQYFWYVPPPTNRHMMHMIHFQQRYSEDHTSRTISKASVTLSLSF<br>SPGEQ  |
| 7 B        | 112   | 279                            | MSPYKGVAGPASRCGECGGARKLRDASKHGAPREGRHCGSSEEVE  |
| / B        |       | i i                            | RQECVTACSL AVRETET   |
| 8 B        | 198   | 405                            | EKEEEENVEEILRGGDWPNRQVSMGCWDTVGDVEIDRNKHIHKKRK MSHRAWPPCCTGPNASQVPLVSMVAKAFLANSTEVLESFKLARES   |
| 9 B        | 346   |                                | MSHRAWPPCCTGPNAPSQVPLVLLEUVSNV TOSTEVLESFKLARES<br>AEGREKTMSSDDEDCSAKGRNRHIVVNKAELANSTEVLESFKLARES<br>WELLYSLEFLDKEFTRICLAWKTDTWLWLRIFLTDMIIYQGQYKKAIASI<br>WELLYSLEFLDKEFTRICLAWKTDTWLWLRIFLTDMIIYQGQYKKAIASI<br>HHLAALQGSISQPQITGQGTLEHQRALIQLATCHFALGEYRRREGMGI<br>TGAVAVDLLKVVKDMIQGIGNLTTLFHFPLLGDF<br>MILLSCSSWVLVASCWQTLSDIFSGGKTKCISLGCQINSALTSFHTALE<br>JAVDQREIQHVCLYEIGWCSMIELNLKDAFDSFERL  |
|            | 1 348 | , 000                          | VINLES   |

| 20100 D | 1   | 714 MAF                                | GLGAIWGVLILTCLLPVNQLLTALPVDVLGSLGELSSPVVSAFALFP<br>FYQFGWKQSLIAAVVVLMTRVVVVRYFPHLNPESIEIFIGMVMLLGI   |
|---------|-----|--|--|
| 30468 B |     | ILVAI                                  | FYQFGWKQSLIAAVVVLIMITED TO DIIVAII DYIAIVGAI IAAVASMKIF  |
|         |     |  | IDLRHRDENDIDASGLSVFEER ISRIINNLF 1777 VO<br>EVSIFTLEKAYSAGVTPEQSQTLINQAALAEFMRGLGFVPLIATTAL<br>VYAVAGFTFVYAVDYLSPNPMVAAVLGAVVI   |
|         |     | 1007 VII 6                             | SRMYGNLPIEYGADGAGSGNCGTPCRVTPTERRMEVYSISIWMMT  |
| 30469 B | 166 | PCV<br>CAS<br>DSH<br>SDC<br>VLT<br>GV/ | SRMYGNLPIEYGADGAGSGNUGI PORVIT LINNEDWPLKI<br>YEHMMGSARNASYCDGITSRRIYLIWGMVGENQVFDDMDQWPLKI<br>YEHMMGSARNASYCDGITSRRIYLIWGMVGENQVFDDMDQWPLKI<br>SCGHKRIRYVMILSAFSLEGKVAVVMVVILDWKVVNVDFVMLITEYAA<br>KURLITHPLPWLTPSGVDGEKRQNSVAVFRNRKYAHKSRQRRRSH<br>KURLITHPLPWLTPSGVDGEKRQNSVAVFRNRKYAHKSRQRRRSH<br>JUETSGYLDLQPEMSSAELTEKLVGPSRAANTTPSSVTIRTHDDQ<br>JUETSGYLDLQPEMSSAELTEKLVGPSRAANTTPSSVTIRTHDDQ<br>JUEVWKLPARIWSLKKLHYSRPNSGGATRHRKTILSNTGDDLDVI<br>GLIVWKLPARIWSLKKLHYSRPNSGGATRHRKTILSNTGDDLDVI<br>GLIVWKLPARIWSLKKLHYSRPNSGGATRHRKTILSNTGDD<br>GASQMRPYRNWRDARLMFNQTRGDRARYLKLARTNAATALTSKLS<br>JOSQMRPYRNWRDARLMFNQTRGDRARYLKLARTNAATALTSKLS<br>STVHRD  |
| 1 1     | 1   |  | PNVSGNPVIKYFNYLYTYKMPGDIKNWVDAHMNCEDIAMNFLVAN  |
| 30470 B | 72  | VT<br>YQ<br>ET                         | GKAVIKEAGYKRPODROSSBEPGI EZIR<br>ILEELEKVFOKTHYPDVYAREQLAMRTDLTEARVQAVIRQRAGNARK<br>NRAQVDVLVEFTTKFQQRTPQRNMVRNGIRPPTAPK   |
| 1 1     |     | 1000 140                               | SALITSSTPALGGRSLPLCAGPAGYTAAVYAARANLQPVLITGMEKG  |
| 30471 B | 1   | G(                                     | OLTTTTEVENWPGDFNDLTGI ELITETTEVENWPGDFNDLTGI ELITETTETTETTETTETTETTE |
| 1       |     | IRI                                    | RDGFRAEKILIKRLMDKVENGMILLTTMALEEGOLELETII PNPRPSPKFKNG   |
|         |     | LS                                     | DISDNIESLDVAGLEVAIGHSPNIAIREGULEUFSIDYAELLQHFEK<br>SCFPGKIVTVPFPTNINRKIKDSLKAAPKSQKADSPSIDYAELLQHFEK<br>DINKHLEVRHQRSGRGDHLDRRVVLTGLARRAHRVVP<br>DINKHLEVRHQRSGRGDHLDRRVVLTGLARRAHRVVP   |
|         |     |  | IELGRGIKGLIGHTQSCRLAARTVANRIAEDLKHGAGRLHRLQSAFQR   |
| 30472 B | 1   | S                                      | IELGRGIKGLIGHTGSCRLARI (VARNIABELDINGSCHAR) PEEDTNVVRHNVPGAAHSRTYRFTFSGIAGGWITTQLAIKKRQCTRA PEEDTNVVRHNVPGAAHSRTYRFTFSGIAGGWITTQLAIKKRQCTRA IKQTAFMDSMKSDMGGAATVTGALAFAITRGLNKRVKLFLCCADNLIS IKQTAFMDSMKSDMGGAATVTGALAFAITRGLNKRVKLFLCCADNLIS INAFKLGDIITYRNGKKVEVMNTDAEGRLVJADGLIDASAQKPEMIIDAA ILTGAAKTALGJASMHCSANVGEKGDVAVFFGLSGTGKTTLSTDPKRR ILGDDEHGWDDD   |
|         | 1   |  | MAVAAAALSLLLLLILSRTNEFDLRVFIQPQHDSGEDTYPYWSQIIVTIII  |
| 30473 B | 1   |  | TWDQMAPTSKGYHEUSMIST JELOSIIICATION TOVAEYRRDCGSRFR<br>GLHHIKAENRLSNAYTSATSPPLKKLPLARTANYDVAEYRRDCGSRFR<br>GYAIFTGHFFHFIARHPTPPWRTNWRCNWFCRRSPARKAAALAKASV<br>SYAIFTGHFFHFIARHPTPPWRTNWRCNWFCRRSPARKAAALAKASV<br>NKVFFIQPTPQFVIGQTEAAGIRIISQLPLRTHIPGYGAAAFAQPGRRAIA<br>MTINREPQRG   |
|         |     |  | MKIPSLVGPDGKTSLREYAGYHGGGGGFGGQLRGWNPPSESADAAL   |
| 30474 B | 1   | 3822                                   | MKIPSLVGPDGKTSLREYAGYHGGGGGFAGN<br>LPNFSRGNARADDLVRNNGYAANAVOLHQDHIVGSFFRLSYRPSWRY<br>LGNEEDSRAFSRDVEAAWNEYAEDDFCGIDAERKRTFITMMIREGVAM<br>HAFNGELCTQATWDSDSTRLFTGFKMYSPKRVSNPNNIGDTRNCRA<br>GVKINDSGAALGYYYSDDGYPGWMAQNWTYIPRELPGGRPSFIHVFE<br>JMEDGQTRGANAFYSVMEQM  |

|             |       |        | 39-41 199 204-207 322-323 549-551 585-589  |
|-------------|-------|--------|--|
| adult brain | GIBCO | AB3001 |  |
| addic bias  |       |        |  |
|             | 1     |        |  |
| 1           |       |        |  |
|             | 1     |        |  |
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|             |       | 1      |  |
| 1           | 1     | 1      |  |
| 1           | 1     | 1      | 7263-7266 7501-7503 7506 7714-7719 7608-7609 7676-7677 7684-7690 7714-7719   |
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|             | - 1   | i      |  |
|             | 1     |        | 8472 8554-8556 8993-037<br>9072-9076 9397-9398 9426-9428 9435-9436<br>9072-9076 9397-9398 9426-9428 9435-9536                              |
| 1           |       |        | 9072-9076 9397-9398 9426-9426 9503 9535-9536<br>9451-9452 9455-9456 9491-9496 9503 9535-9536   |
| 1           | 1     | 1      | 9451-9452 9455-9456 9434-9649 9663-9664<br>9577-9578 9582-9585 9646-9649 9663-9669<br>9912-9913 9915-9916 9935-9956 9966-9969              |
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|             | 1     | 1      | 15340-15341 15347 15413-15415<br>15658-15662 15666-15667 15678-15679 15790-  |
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|             | 1     | 1      | 18069 18136-18137 18243-1831 18733-18735 18777-<br>18623-18625 18644-18646 18733-18735 18777-<br>18781 18828-18831 18859-18865 18899-18902 |
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|             | 1     | 1      | 21199-21202 21264-21267 21272-21338-21542  |
|             | 1     |        | 21199-21202 21264-2120 212411 21538-21542<br>21281 21400-21402 21405-21411 21538-21542<br>21562-21567 21613-21619 21623-21628 21775-       |
|             | 1     |        | 21562-21567 21613-21619 21623 22086-22089  |
|             | 1     | 1      | 21783 21857-21861 22057-22055<br>22101-22102 22106 22128-22134 22154-22157   |
| 1           |       |        | 22101-22102 22106 22126-2213   |
|             |       |        | 8532   |

TABLE 18

| 27013-27015 2736-27772 27805-27808 27818-<br>27658-27661 27768-27772 27805-27808 27818-<br>27823 27898-27908 28031-28034 28066-28097<br>27823 27898-27808 28303-28307 28483-28485 28598 |
|---|
|---|

TABLE 19

| ID | ACCESS-<br>ION<br>NUMBER |  | %<br>IDENTITY |
|----|--------------------------|--|---------------|
|    |                          |  | 1 29.73       |

|        |             | 2 - ille corille atrophin-1  | 51   | 29.73  |
|--------|-------------|--|------|--------|
| 3379 A | J133271     | Gorilla gorilla atrophin-1   | 149  | 27.536 |
| 3380 A | J133271 C   | Gorilla gorilla atrophin-1   | 149  | 27.536 |
|        |             | Gorilla gorilla atrophin-1 Mus musculus Pro-Pol-dUTPase polyprotein                      | 344  | 60.825 |
|        |             | Mus musculus Pro-Pol-dOTP ase polyprotein Mus musculus Pro-Pol-dUTPase polyprotein       | 634  | 87.85  |
| 3384   |             | Mus musculus Pro-Poi-do Frase polyprotein  | 369  | 82.353 |
|        |             | Mus musculus Pro-Pol-dUTPase polyprotein   | 523  | 38.776 |
|        |             | Mus musculus Pro-Pol-dUTPase polyprotein   | 467  | 68.807 |
| 3388   | Y12713      | Mus musculus Pro-Pol-dUTPase polyprotein  Mus musculus Pro-Pol-dUTPase polyprotein       | 237  | 70     |
| 3390   | AL049758    | Homo sapiens dJ437M21.1 (novel protein)  | 344  | 47.682 |
| 3391   |             |  | 1266 | 85.965 |
| 3392   | Y09443      | Homo sapiens alkyl-dinydroxyacetonephosphare   |      |        |
|        |             | synthase precursor   | 1243 | 92.991 |
| 3393   | Y09443      | Homo sapiens alkyl-dihydroxyacetonephosphate   | 1    |        |
| ••••   |             | synthase precursor   | 1959 | 91.875 |
| 3394   | X79536      | Homo sapiens hnRNPcore protein A1  | 593  | 51.261 |
|        | X79536      | luomo capiens hnRNPcore protein A1   | 315  | 95.652 |
| 3396   | X79536      | Homo sapiens hnRNPcore protein A1  | 1486 | 98.4   |
| 3397   | X79536      | Homo sapiens hnRNPcore protein A1  | 8177 | 100    |
|        | U34360      | Homo sapiens LAF-4   | 205  | 59.322 |
|        |             | Homo sapiens LAF-4   | 165  | 30.46  |
|        | 111022524   | Schizosaccharomyces pombe serine-rich protein  | 281  | 40.764 |
| 340    | I AI 117470 | Homo sapiens hypothetical protein  | 313  | 69.231 |
| 340    | 2 U22376    | Homo sapiens hypothetical protein  Homo sapiens alternatively spliced product using exon | 313  | 00122  |
| 340    | Z CZZO. G   | 134  | 2454 | 70.623 |
| 240    | 3 L11672    | Homo sapiens zinc finger protein   | 288  | 46.939 |
| 240    | 4 A R 00662 | 8 Homo sapiens KIAA0290  | 183  | 36.029 |
| - 440  | 0 4000000   | o Homo saniens KIAA0290  | 604  | 64.216 |
|        | = 4144040   | A Illiamo saniens hypothetical protein   | 219  | 53.684 |
|        | 0 41 44042  | 4 ILlomo saniens nyboti leticai proteir  | 204  | 94.595 |
| 0.40   | 0 41 44042  | A lillomo sabiens hypothetical protein   | 3778 | 97.879 |
| 340    | 9 AL 11012  | A ILlama caniens hypothetical protein  | 820  | 80.66  |
| 34     | 11 X56932   |  |      | 10     |
| 34     | 12 X56932   | Homo saniens 23 kD highly basic protein  | 505  | 98.51  |
|        |             |  | 1260 | 39.72  |
|        | 13 X56932   |  | 289  | 26.62  |
| 34     | 14 AF01014  | Homo sapiens neutrina thread pro-  | 257  | 26.62  |
| 34     | 15 AL1328   | preliminary prediction   |      | 92.30  |
|        |             | Homo sapiens herpesvirus associated ubiquitin-specific                                   | 867  | 92.30  |
| 34     | 16 Z72499   |  |      | 00.74  |
|        |             |  | 557  | 32.71  |
| 34     | 17 Z72499   |  |      | 00.00  |
|        |             | 1  | 7326 | 99.63  |
| 34     | 118 Z72499  | protease (HAUSP)   |      | 1      |

TABLE 19

|                            |  | Day CTB hinding protein: RanBP6  | 1020 | 86.188                      |
|----------------------------|--|--|------|-----------------------------|
| 30403                      | AF039023                               | Homo sapiens Ran-GTP binding protein; RanBP6   | 7063 | 97.922                      |
| 30404                      | AF039023                               | Homo sapiens Ran-GTP binding protein; RanBP6  Homo sapiens Ran-GTP binding protein; RanBP6 | 1536 | 95.102                      |
| 30405                      | AC002400                               | Homo sapiens Gene product with similarity  | 1    |                             |
|                            |  | binding enzyme   | 341  | 90.741                      |
| 30406                      | AC002400                               | Homo sapiens Gene product with similarity to Ubiquitin                                     | 1    |                             |
|                            |  | binding enzyme   | 3437 | 98.876                      |
| 30407                      | AC002400                               | Homo sapiens Gene product with similarity to Ubiquitin                                     |      |                             |
|                            | 1                                      |  | 344  | 60.63                       |
| 30408                      | 8 M24903                               | Homo sapiens gamma-glutamyltransferase 1 (EC   |      |                             |
|                            |  | 2.3.2.2)   | 3687 | 100                         |
| 30409                      | 9 M24903                               | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1    |                             |
|                            |  | 2.3.2.2) Learn-Heaperforage 1 (FC  | 3633 | 98.611                      |
| 3041                       | 0 M24903                               | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1    |                             |
|                            |  | 2.3.2.2)   | 46   | 40.909                      |
| 3041                       | 1 M24903                               | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1 1  |                             |
|                            |  | 2.3.2.2)   | 1311 | 85.156                      |
| 3041                       | 12 M24903                              | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1 1  |                             |
|                            |  | 2.3.2.2)   | 1369 | 95.671                      |
| 3041                       | 13 M24903                              | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1    |                             |
|                            |  | 2.3.2.2)   | 2808 | 79.701                      |
| 304                        | 14 M24903                              | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1    |                             |
|                            |  | 2.3.2.2) Literarytransferase 1 (FC   | 3357 | 96.701                      |
| 304                        | 15 M24903                              | Homo sapiens gamma-glutamyltransferase 1 (EC   | 1 1  |                             |
|                            | 1                                      | 2.3.2.2) (FC:  | 2944 | 82.89                       |
| 304                        | 16 M24903                              | Homo sapiens gamma-glutamyltransferase 1 (EC   |      |                             |
|                            |  | 2.3.2.2)   | 80   | 36.364                      |
| 304                        | 17 U02390                              | Homo sapiens CAP2  | 346  | 59.66                       |
| 304                        | 118 U02390                             | Homo sapiens CAP2  | 2204 | 91.03                       |
|                            |  | Homo sapiens CAP2  | 137  | 55.26                       |
|                            |  | Homo sapiens p21-activated kinase 3  | 260  | 78.18                       |
|                            |  |  | 2883 | 87.18                       |
|                            |  |  | 518  |                             |
|                            |  |  | 376  |                             |
|                            | A F4040                                | eo Mus musculus CAMP Inducible 1 protein   | 332  |                             |
|                            |  |  | 59   |                             |
|                            |  |  | 68   |                             |
|                            | 104040                                 | NO IMUS MUSCUIUS CAMP INQUOIDIE I PIOCEII  | 5.   |                             |
|                            |  |  | 6    |                             |
|                            |  |  | 132  |                             |
|                            |  |  | 283  |                             |
| 30                         | 0435 AF121                             |  | 561  | 4                           |
| 1 30                       | 0436 U1719                             |  | 384  |                             |
| 20                         | 0436 U1719                             | F. Homo saniens A-kinase anchor protein  | 72   | 1                           |
| 30                         |  |  |      |                             |
| 30                         | DE 47 V 0974                           |  |      |                             |
| 30                         | 0547 X9874                             | 2 Homo saniens RNA helicase  | 299  |                             |
| 30                         | 0547 X9874<br>0548 X9874               | 3 Homo sapiens RNA helicase  | 68   | 90.5                        |
| 30<br>30<br>30             | 0547 X9874<br>0548 X9874<br>0550 X9874 | Homo sapiens RNA helicase Homo sapiens RNA helicase  | 12   | 90.5<br>75 75.9             |
| 30<br>30<br>30<br>30<br>30 | 0547 X9874<br>0548 X9874               | 3 Homo sapiens RNA helicase 3 Homo sapiens RNA helicase 3 Homo sapiens RNA helicase        | 12   | 99 90.5<br>75 75.9<br>57 21 |

|                |       |     |          |          | AMINO ACID SEQUENCE ENCODED BY THE NUCLEOTIDE  |
|----------------|-------|-----|----------|----------|--|
| EO T           | ме    | Pı  | redict-  | Predict- | AMINO ACID SEQUENCE ENCODED BY INE NOOMAND SEQUENCE OF THE CORRESPONDING SEQ ID NO. (A=Alanine, SEQ ID NO. (A=Ala |
|                | th    |     | d beg-   | ed end   |  |
| >              |       |     | nning    | nucleo-  | C=Cysteine, D=Aspartic Acid, D=Wistidine,  |
| o.             | od    |     |          | tide     | F=Phenylalanine, G=GIycine, M=Methionine,  |
| - 1            |       |     | ucleo-   | loca-    | I=Isoleucine, K=Lysine, L=Leucine, N=Neginine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, N=Asparagine, N=Proline, N=Tryptophan,  |
|                | 1     |     | ide      |          | N-Asparagine, P-Proline, Q-Glutamine, K-Alguna   |
|                | l     | 1   | oca-     | tion     | N=Asparagine, P=Proline, Q=Glucamine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, S=Serine, T=Threonine, V=Stop Codon, /=possible   |
|                | 1     | ١t  | ion      | corres-  | S=Serine, T=Threonine, V=Valine, w=11770000000000000000000000000000000000  |
|                | 1     | 10  | orres-   | ponding  | Y=Tyrosine, X=Unknown, x=gtop teach, nucleotide deletion, \=possible nucleotide  |
|                | 1     |     | onding   | to last  | nucleotide deletion, (-possess   |
|                | 1     |     | o first  | amino    | insertion)   |
|                | 1     |     |          | acid     |  |
|                | 1     |     | mino     | residue  | 1  |
|                | 1     |     | acid     | of amino |  |
|                | 1     |     | residue  |          |  |
|                | 1     | 10  | of amino | acid     |  |
|                | 1     | -17 | acid     | sequ-    |  |
|                | 1     | ١.  | sequ-    | ence     |  |
|                | 1     |     | ence     | 1        | TOWAY I PEWCDON*   |
|                | +-    |     | 239      | 322      | MGGALLKEPILSPGGGKGKIFFWGPQN* SVIA*SCRASVASKQS*PFLLPSACARPHA\STVDAPASGGAPRASSP\SSD SVIA*SCRASVASKQS*PFLLPSACARPHA\STVDAPASGAPRASSP\SSD  |
| 1              | C     |     |          | 2130     | SVIA*SCRASVASKQS*PTLLPSACARPHA\SIVDIRGEOGPGARGRSCSPSSSERH  |
| 2              | A     | - 1 | 1441     | 2130     | CLWSTSSSSTPLSASASSS/SPFSFREE CALCER CALCER AND ASSATPALAQST  |
|                | 1     | - 1 |          | 1        | CLWSTSSSSTPLGASASSS/SPPSYMPAUAAGSGV<br>VRRVSAARQAGASAGGRQAGLAGRSGLSA/SRSSARASSSATPALAQST<br>VPSSESECAPLKSRSGLTSSLSKPAS*ATLGKKGSGSSWRFPPESIHGRHPL<br>VPSSESECAPLKSRSGLTSSLSKPAS*ATLGKKGSGSSWRFPPESIHGRHPL   |
|                | 1     | - 1 |          | 1        | \ macreerChpt.KSRSGLTSSLSAFAS ATZON  |
|                | - 1   | - 1 |          | 1        | SASCWNKSVAAAAAPTGATAPPKAGP SASCWNKSVAAAAAPTGATAPPKAGP  |
|                | - t   | - 1 |          |          | SASCWNKSVAAAAAPTGATAPPKAGP MGPTIPDXSXFFWRKPITWMPTWEGTSNVGPQPLSSSKSLHSXRGHPAPIPT  |
| 3              | - c   | - 1 | 36       | 236      | MGPTIPDXSXFFWRRFITHIZ  |
| 3              | ١٠    | - 1 |          |          | GQAGPRDSGPGASP* GGGKQIPFKGGKFKWGPGPVLKKGEREKPGGNPKKTPWKKASSRPAPRIHPC   |
|                |       |     | 109      | 300      | GGGKQIPFKGGKFKWGPGPVLKKGEKEKIOOM   |
| 4              | A     | - 1 | 109      | 1500     | PRESENTATION OF THE PROPERTY.  |
|                |       | _   |          | 74       | FPKGFFFGYPRFFPFPFLNPGPG FPKGFFFGYPRFFPFPFFLNPGPG   |
| 5              | A     |     | 2        |          | FPKGFFFGYPRFFPFFPPFINPGPG  EHSGVRQALCFGTASQRPSQQPAPSGPGPPGEPG*ERLCASHKAFISHKQSH  EHSGVRQALCFGTASQRPSQQPAPSGPRTOTLSLTSQPTACSENSQ  |
| 6              | A     |     | 27       | 375      | EHSGVRQALCFGTASQRPSQQPAPSGPGPPGEFG ERGCADATE STATES OF TACSENSQ *SPQ*PCQAGVTLSRLQTTNSPRPHSQKGLRGPRTQTLSLTSQPTACSENSQ   |
| 1              | - 1   |     | }        |          | *SPQ-FCQRC+=====   |
| ١              | - 1   |     | 1        |          | GSQPSPKRTLS  KKEGSLCDEYWNPAANLINVCSLFLRQGPRLALMQGEPVDKGCLGVLLENK*  KKEGSLCDEYWNPAANLINVCSLFLRQGPRLALMQGEPVDKGCLGVLLENK*  |
| <del>-</del> - | - B   | _   | 50       | 204      | XKEGSLCDEYWNPAANLINVCSLFLRQGFRHALIGES  ATTVSVFPFTAKLLERPGLHLLVFLPNLQFPLQPLVS*LALLRGSTLTKQVP  |
| 7              | - A   | _   | 379      | 623      | ATTVSVFPFTAKLLERPGLERBUT BY LOCAL  |
| 8              | A     |     | 13/3     |          | SAPDKPLLVSPSPAKHPPVPPSCGPGLQG<br>SAPDKPLLVSPSPAKHPPVPPSCGPGLQG<br>SAPDKPLLVSPSPAKHPPVPPSCGPGLQG<br>SAPDKPLLVSPSPAKHPPVPPSCGPGLQG   |
|                |       |     | <u> </u> | 366      | SAPDKPLLVSPSPAKHPPVPPSCGPGLQG  XHPGDGFRPNQEGDERPARKKTWVRDGGPHQGLFRSFHPQFFSRPSRATAHV  |
| 9              | _   E | 3   | 185      | 300      | PAVYFSVEWX*  |
| 1              | - 1   |     |          |          | PAVYFSVEWX* WLPPNPGRRREARQEEDLGPGWWAPSGPLPQLPSAVLQPTQPGHGPRASL**   |
| 10             | 1     | Ā   | 29       | 308      | WLPPNPGRRREARQEEDLGPGWWAFSGT TO SUCFSFADKEGSLCDEYWNPAA/KPH*RLQPLPSTRPEISPL SVCFSFADKEGSLCDEYWNPAA/KPH*RLQPLPDEKSSPLAGLSSPFPWFGRKF  |
| 1-             | - 1   |     | 1        | 1        | SVCFSFADKEGSLCDEYWNPAA/KPH-KUFIE-<br>TAGTWAVASLGRLKNCGWKLRKEALMGPTIPDPKSSPLAGLSSPFPWFGRKF<br>TAGTWAVASLGRLKNCGWKLRKEALMGPTIPDPKSSPLAGLSSPFPWFGRKF<br>TAGTWAVASLGRLKNCGWKLRKEALMGPTIPDPKSSPLAGLSSPFPWFGRKF  |
| 11             | -+-   | A . | 663      | 1270     | TAGTWAVASLGRLKNCGWKLRKEALWGF I FPDF ROTE ITLECPTWERDPRNVGPPAPSPARKSLPQPTGTTLQPYSPRDKAGPKKTLGF ITLECPTWERDPRNVGPPAPSPARKSLPQPTGTTLQPYSPRGAVEPSVSAC  |
| 111            | - 14  | -   | 1 303    | 1        | ITLECPTWERDPRNVGPPAPSPARKSLPQPTGTTG<br>RG/APL*VRRTRPLN*WTPADLGVRTRGAGPLPDPAGTLRPRGAVEPSVSAC<br>RG/APL*VRRTRPLN*WTPADLGVLAHPTVLSINVFPVLNQKKKKK  |
| 1              | - 1   |     | 1        | 1        | RG/APL*VRRTRPLN*WTPADLGVKI KONGO ANDTVLS INVFPVLNOKKKKK  |
|                | - 1   |     | 1        | 1        | GKWAPSPTSQGCCEGRCDAVPKHEGHAMI I CSPEOAVELSALLAQTKI   |
|                |       |     |          | 715      | WRWRWRRKPTARTASTRHIFFLHIKEALLAGHLLCGF BOAT SAFVOVIOIV  |
| 12             | : 1   | A   | 190      | 1,13     | WRWRWRRKPTARTASTRHIFFLHIKEALLAGHDLCST<br>GDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQASAEYQVLQIV:<br>GDYNQNTAKYNYEELCAKELSSATLNSIVAKKELEGTSQASAEYQVLQIV:   |
| 1              | - 1   |     | 1        | 1        | GDYNQNTAKYNYEELCAKELSSATINSIVAKAKELISSA<br>AMENYGIEWHSVRDSEGHKLLIGVGPEGISICRDYFSPINRIAYPVVQMAT   |
| 1              | - 1   |     | 1        | 1        | SGKNYYLTVTMESVNSIEL  |
| - 1            | - 1   |     | į.       |          | SGKNVYLTVTMESVNSIEL  KLTILDCQFTG*QR*KFNG*NLRNR/HSPSRWDGAKPLYKALKL*SSSSSV  KLTILDCQFTG*QR*KFNG*NLRNR/HSPSRWDGAKPLYKALKL*SSSSSV  |
| 13             | , +   | A   | 270      | 713      | KLTILDCQFTG*QR*KFNG*MIRNN/HSPSRWDGANC<br>AFIFIFTRSRLRAYLFSFAH/LRRPLLAGHLLCSPEQAVELSALLAQTKFG<br>AFIFIFTRSRLRAYLFSFAH/LRRPLLAGHLLCSPEQAVELSALLAQTKFG  |
| 1 1            | ۱ -   | ^   | 12.5     | 1        | AFIFIFTRSRLRAYLFSFARI  |
| - 1            | - 1   |     | 1        | 1        | YNONTAKYNYEELCAKELSSATINGT THE TERMINITURE TO FULL FULL FOLLOWS LT   |
| L              |       |     |          | 1968     | REMGFRHVGQTGLELLTSGDLPTSASQSAGIIGVSHITHTKTCCDDNI.HISSF   |
| 1.             | 4     | Α   | 1575     | 1368     |  |
| 1              | - 1   |     | 1        |          | SPGLECSGIISARCSTADARCSTA   |
| -              | 1     |     | 1        |          | GASPCWPGCS*TPELKRPAHPCKDQLSH<br>KVSHVYLFLHRHGNHPISQTFPHLSPLSIPQNCHCHHGPFSMSCWRIKYLC<br>KVSHVYLFLHRHGNHPISQTFPHLSPLSIPQNCHCHHGPFSMSCWRIKYLC   |
| +              | .5    | A   | 185      | 721      | KVSHVYLFLHRHGNHPISQTFPHLSPLSIPQRCHARGINIVKMAILP/KI<br>QLTRDVKDLFKEN*KPLLSKIKEDTNKWKNIPCSWIGRINIVKMAILP/KI  |
| 1 -            | . э   | 1 ~ | 1 -00    | l        | QLTRDVKDLFKEN*KPLLSKIKEDTNKWKNIFCS#20KT<br>EKTTLKFIWNQKRACIAKTILSQKNKAGDITLPDFKLYYKATVTKTAWE\(()   |
| 1              |       | ١   | 1        | 1        | EKTTLKFIWNQKRACIAKTILSQAMASSITZI<br>RDIDQWNRIEPSEITPHIYNYLIF   |
|                |       |     |          | ı        | CURVETED CETTENTYNYLLE   |

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TABLE 20

| 5818 F       | A            | 2 :    |      | MHINPANKSLPPTFGPATLFNHFSSLPDSSQVPANQGWGDGPLSRVATDAS PTVQSAPLGNSVLGHLENMHPDNSKAPGFRPPSQRVSTSPVGLPSIDPSGSS PSSSSAPLASFGGI FGTRVFLQGPAPVGTPSFNRQHFSPHPWTSASNSSTSA PSSSSAPLASFGGI FGTRVFLQGPAPVGTPSFNRQHFSPHPWTSASNSSTSA GWSFGVNAVSEGLSGWSQSVMGNHPMIQQLSDPSTFSGHQPMERDDSGMVA GWSFGVNAVSEGLSGWSQSVMGNHPMIQQLSDPSTFSGHQPMERDDSGMVA PSNIPHGPMASGFVDFSKGLPISMYGGTI I PSHPOLADDVGGPLFNGLHNPD PANNDMIKLVIQNSTECTDAQI IMPGTWAPHIGNMHLKYVN GGTESTRYAVQLINALIQDPAKELEDLI PKNHI RTPASTKSI HANFSSGVGT TAASSKNAFPLGAPTLVTSQATTLSTFQPANKLMKNYPTNVRSSFPVSLDLA VPHPHFALLAAQTMQQI HPRLPMAQFGGTFSPS PNTWGFFVPVNFGNTN SSPKINNTSRLPMQNGTVLPSESSGLATASCPITVSSVAASQOLCVTNTRT PSSVRKQLFACVPKTSPFATVISSVTGTSSLPSVSAPITSGQAPTTFLPA STSQAQLSSQKMESFSAVPPTKEKVSTODQPMANLCTPSSTANSCSSSASNT SGAPGTHPSSSPTTFTSSNTQEBAQPSSVSDLSPMSMPFANSEAPAPTLTSP FGAPETHPSSSPTTFTSSNTQEBAQPSSVSDLSPMSMFPANSEAPAPTLTSP FGWAADNDGTSNLPGLAVPARFVSHRWQPRGSFYSMVPNATIHODPQSIFVT NPVTLTPPGGPPAAVQLSSAVNINNGSQMINFANKSLPPTFGPATLFNHFS SLFDSSQVPANQGWGGDFLSSKVATDASFTVQSAFLGNSVLGHLENMHPDNS SLFDSSQVPANQGWGGDFLSSKVATDASFTVQSAFLGNSVLGHLENMHPDNS SKAPGFRPPSQRVSTSPVATSAPPTLGQPKVSSKARDRSP |
|--------------|--------------|--------|------|---|
| 5819         | A            | 1      | 394  | QGGSVAQAPAGTSFVAPVGHSGIWSFGVNAVS SSLFDSSQVPAFQRVSTSPVGLPSIDPSGSSPSSSAPLASFSGIPGTRVFL QGPAPVGTPSFNRQHFSPHBWTSASNSSTSAPPTLGQPKGVSASQDRKIPPP QGPAPVGTPSFNRQHFSPHBWTSASNSSTSAPPTLGQPKGVSASQDRKIPPP  |
| 5820         | A            | 2      | 1785 | IGTERLARIRQGSVAQAPAGTSFVAP  OLFACTVEKTSPPATVISSVTSTCS LIPSVSSAPITTSQAPTTFLPASTSQAQ  OLFACTVEKTSPPATVISSVTSTCS LIPSVSSAPITTSQAPTTFLPASTSQAQ  LSQKMESFSAVPPTKEKVSTQDQPMANLCTPSSTANSCSSSASNTPGAPET  LSGKMESFSAVPPTKEKVSTQDQPMANLCTPSSTANSCSSASNTPGAPET  HSSSPTPTSSNTQEEAQPSSVSDLSPMSPFASNSEPAPITLTISSPRIMADA  HODTSHLPQLAVPAPRVSHEMQPGRSFYSMYPMATIHDDPQSIFVTNPVTLT  PPQGPAAVQLSSAVNINNGSQMHINPANKSLPPTFGPATLTHIFFSLFDSS  QVPANQGMGDGPLSSVATDASFTVQSAFLGNSVLGHLENMHPDNSKAPGFR  PPSQR\USTSPVGLSSVATDASFTVQSAFLGNSVLGHLENMHPDNSKAPGFR  PPSQR\USTSPVGLSSVATLPSITERLARILQGSVAQAPAG\TSFVAPVGH  LG\QPKGSQCQSRIRKGVLPPIGTERLARILQGSVAQAPAG\TSFVAPVGH  SG\IWSFGVNAVSHCHPMANSGVMG\NHPMARNNFSGPKAHFSQHQPMER  DDSGWAPSNIFHQPMASGVTDFSKGLFISMYGGTIFPHPQLADVPGGPLF  NGLHNDDDAMNPHIKVIQNSTECTDAQQVKMA   |
|              | <del>-</del> | 1      | 125  |   |
| 5821<br>5822 | A            | 3 3448 | 3831 | HEKTAPPLKFPKKRGPKPGSAVGGAWSGAVG<br>KNRFCSGVSSNSKSNSCVYYVIDDIDTHTYIHIHTNICHILFFFFFETE<br>SHALSPRLECNGVISAHCNLHPPG\SSDSPASARVAG\TTGTCHHAQLIFF<br>FFVFLVETGFHHAAQAGSCTPDL*STPLGFPKC*DYRF/AAIVPGIFLLH*<br>IR*KVPTLLTDMRNASEYDCDFSTNILDKETTFS*NASLNICLLST*PYEM<br>VTHFKGY*ILDLFFFFILRGSL/SSVTQAGVQWHNLGSLQPLPPGFKQFSCL<br>SLPSSWDYRYQLPRLA/NF/FVFLVETGFHHAAQAGSGTPDLR  |

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TABLE 21

|             | TOTINGE    | HYSEQ   | SEQ ID NOS:  |
|-------------|------------|---------|--|
| TISSUE      | RNA SOURCE | LIBRARY |  |
| ORIGIN      |            | NAME    | 82-83 127 137 157-159 179-181 217-219 287-292  |
|             | GIBCO      | AB3001  | 82-83 127 137 157-159 179-151 1217<br>356-359 460-461 474 507-508 559 577-578 674-   |
| adult brain | GIBCO      |         | 356-359 460-461 474 307 303 848-849 930 957  |
|             |            |         | 675 733-735 780-782 820-821 343-039 1051 1059-<br>1005-1008 1011-1024 1034 1038-1039 1051 1059-  |
|             |            |         | 1005-1008 1011-1024 1034 1038-1038 1142 1181 1186 1063 1068-1074 1083-1084 1098 1142 1181 1186 1063 1068-1074 1265-1267 1339-1340 1363-1364  |
|             | 1          | 1       | 1063 1068-1074 1083-1084 1096 1112<br>1203 1214 1235 1265-1267 1339-1340 1363-1364<br>1203 1214 1235 1265-1267 13412-1414 1451-1453 1455-  |
|             |            | 1       | 1203 1214 1235 1265-1267 1339-1345<br>1373-1374 1402-1403 1412-1414 1451-1453 1455-  |
|             |            | 1       | 1373-1374 1402-1403 1412-1414 1415<br>1457 1462-1470 1491 1497-1499 1514 1517-1519<br>1457 1462-1470 1491 1525 1566-1567 1576-1581   |
|             | 1          | 1       | 1457 1462-1470 1491 1497-1499 1512<br>1522-1524 1531-1533 1535 1566-1567 1576-1581<br>1522-1524 1531-1533 1535 1566-1563 1659-1664   |
|             | 1          | 1       | 1522-1524 1531-1533 1535 1566-1557 1659-1664<br>1609-1611 1625-1627 1644 1651-1653 1659-1664<br>1609-1611 1625-1627 1710-1711 1715 1726-1731   |
|             | 1          | 1       | 1609-1611 1625-1627 1644 1651-1653<br>1668 1702-1703 1707 1710-1711 1715 1726-1731<br>1668 1702-1703 1707 1808 1811 1838 1849-1851   |
|             |            | 1       | 1668 1702-1703 1707 1710-1711 1715<br>1774 1781 1789 1800-1808 1811 1838 1849-1851<br>1774 1781 1789 1800-1808 1885-1886 1909-1910   |
|             | 1          |         | 1774 1781 1789 1800-1808 1811 1336 1909-1910 1853 1857-1864 1876 1883 1885-1886 1909-1910 1853 1857-1864 1875-1980 1982-1984 2013-   |
|             | į.         | 1       | 1941-1942 1963-1965 1775 2175 2178-2185  |
| 1           | 1          | 1       | 2014 2054-2057 2092 2130 2216 2219 2234-2236   |
|             | 1          | 1       | 2194-2196 2200 2202-2203 2221 2361 2375-2377   |
|             | 1          | l       | 2262 2267-2268 2252 2367 2450-2451 2481-   |
| l .         |            | 1       | 2380-2382 2395-2397 2407 2502 2534 2547 2587   |
| 1           | 1          | 1       | 2482 2486 2491-2494 2497-2502 2505 2661<br>2622-2625 2627 2635 2642 2644-2646 2651 2661<br>2622-2625 2627 2635 2642 2644 2646 2651 2661  |
| 1           | 1          | 1       | 2622-2625 2627 2635 2642 2644-2645 2654-2860 2690 2703 2706 2717-2720 2765 2811 2854-2860 2690 2703 2706 2717-2720 2765 2811 2854-2860 2690 2703 2706 2707-2708 2707-2 |
| 1           | 1          | 1       | 2690 2703 2706 2717-2720 2765 2811 2818 2828 3033 2885 2922 2989-2991 2994-2995 3024-3028 3033 2885 2922 2989-2912 2315 3120 3128-3129 3134-   |
|             | ı          | l       | 2885 2922 2989-2991 2994-2993 3128-3129 3134-<br>3036 3096-3097 3112-3115 3120 3128-3129 3134-<br>3036 3096-3097 3112-3123 3123-3236 3268  |
| 1           | 1          | 1       | 13136 3139-3140 310/ 3212 3430-3431 3434   |
| 1           | 1          | 1       | 3136 3139-3140 3167 3219-3221 3230-3431 3434 3396-3397 3399-3408 3427-3428 3430-3431 3434 3396-3397 3399-3408 3490-3482 3490 3500 3519-  |
| l .         | 1          | 1       | 3458 3467 3473-3474 3400 3-53 3557-3570  |
| 1           |            | ł       | 3521 3538-3539 3542 3542 3725 3746-3747 1  |
| 1           | 1          | 1       | 3586-3587 3608-3609 3004 3969-3971 4004- 1   |
| 1           | 1          | 1       | 3806-3813 3828-3832 3033 4110-4112 4144-   |
| 1           | 1          | 1       | 4005 4012-4013 4047 4101-4104 4115<br>4145 4171 4246-4248 4285 4339-4340 4345-4346<br>4145 4171 4246-4248 4285 4317 4428-4433 4524-  |
| 1           | 1          |         | 4145 4171 4246-4248 4285 4333-4346<br>4384 4390 4404-4405 4415 4417 4428-4433 4524-  |
| 1           | 1          | 1       | 4384 4390 4404-4405 4415 4417 4420<br>4525 4568-4569 4586-4590 4816 4843-4845 4866-<br>4525 4568-4569 4586-4590 5039-5040 5100-5101  |
| 1           | 1          | 1       | 4525 4568-4569 4586-4590 4816 4619 5100-5101<br>4868 4872-4873 4990-4991 5039-5040 5100-5101   |
| 1           | 1          | 1       | 4868 4872-4873 4990-4991 5039-304 5460-5461<br>5108-5109 5170-5171 5207 5214-5216 5460-5461  |
| 1           | 1          | 1       | 5108-5109 5170-5171 5207 5215 5787-5789<br>5593-5594 5618-5619 5621-5625 5787-5789<br>5593-5594 5618-5619 157-159 179-181 238 254  |
| ١           |            |         | 5593-5594 5618-5619 5621-3625<br>1-11 52 64 82-83 124 157-159 179-181 238 254  |
| adult bra   | in GIBCO   | ABD003  | 1-11 52 64 82-83 124 157-159 17<br>264-266 287-292 323-325 345 349 364 367-371<br>264-266 287-292 323-325 345 349 364 367-371  |
| 1           | 1          |         | 375 391-392 400-402 400 674-675 693-694  |
| 1           | 1          | 1       | 1578 590-593 598 614 615 769 820-821 825-  |
| 1           | 1          | 1       | 701-702 706-708 743-747 267 271 890-896 900-   |
| 1           | 1          | 1       | 826 840-842 844 848-849 867-871 948-952 957 902 905 913-917 920-928 941-946 948-952 957  |
| 1           | 1          | l       | 902 905 913-917 920-928 941-940 1003 960 963-969 977-989 991-994 998-1000 1003 960 963-969 977-989 1031-1032 1034 1038-1040  |
| 1           | 1          | 1       | 960 963-969 977-989 991-994 998 1038-1040 1005-1008 1011-1024 1031-1032 1034 1038-1084 1089-   |
| 1           | 1          | 1       | 1005-1008 1011-1024 1031-1032 1034 1089-<br>1049-1051 1059-1063 1065-1069 1083-1084 1089-  |
|             | 1          | 1       | 1049-1051 1059-1063 1065-1069 1083 116-1121 1090 1094-1098 1100-1101 1103-1104 1116-1121 1090 1094-1098 1108-1108 1167-1170 1174-1178  |
| 1           | 1          | 1       | 1090 1094-1098 1100-1101 1103-1170 1174-1178 1123-1124 1128 1146-1148 1167-1170 1174-1178 1123-1124 1128 1216 1219 1222-1226 1234  |
| 1           | 1          | l l     | 1123-1124 1128 1146-1148 1167-1149 1222-1226 1234 1186-1194 1203 1214 1216 1219 1222-1226 1234 1186-1194 1203 1214 1216 1219 1222-1283 1300-1301   |
| 1           | 1          | 1       | 1237 1242-1247 1261-1267 1262 1351-1352 1360-  |
| 1           | 1          | 1       | 1309-1311 1314-1320 1309-1389 1401-1404  |
| 1           |            | 1       | 1362 1370 1373-1374 1373 1455-1456 1473  |
| 1           | l          | 1       | 1435-1436 1447-1446 1436 1517-1520 1531-1533   |
| 1           | 1          | 1       | 1491-1496 1501-1502 1513 1560 1562-1567  |
|             | 1          | ł       | 11535 1543-1544 1545-1552 1502 1613-1614 1619-   |
|             |            | 1       | 1574-1577 1584 1589-1590 1597 1613 1620 1624-1627 1633-1634 1650 1654-1657 1659-   |
|             |            |         |  |

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## TABLE 21

| \$ 508 564-566 599-606 609-611 815-819 840-842 848-849 963 990 1034 1040 1051 1100 1121 1203 1265-1267 1270-1272 1295-1297 1370 1405-1409 1446-1470 1462-1470 1486-1487 1491 1517-1519 1534 1549 1562-1565 1624 1669-1671 1704-1706 1714 1743-1744 1752 1798 1814-1815 1817-1818 1849-1743-1744 1752 1798 1814-1815 1817-1818 1849-1743-1744 1752 1798 1814-1815 1877-1818 1849-1743-1744 1752 1798 1816-1803 12051-2061 2092 2133 2168-2175 12052-2062-2062-2062-2062-2062-2062-2062- |
|--|
|--|

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| Q ID | ACCESSE  | DESCRIPTION   | MITH-<br>ATERMAN | %IDENTITY |
|------|----------|---|------------------|-----------|
| ):   | NUMBER   |   | CORE             | 33.906    |
|      |          | Leishmania major  | 91               | 33.500    |
|      | AJ243460 |   |                  | 34.694    |
|      |          |   | 19               | 34.054    |
|      | U42580   |   |                  | 1         |
|      |          | A41R, corresponds to Genbank  |                  | 1         |
|      | 1        |   |                  | 703       |
|      |          |   | 48               | 34.783    |
| 5    | U42580   | paramecium bursaria chiofere<br>1 PAPK (17X); similar to PBCV-1 ORF |                  | 1 1       |
| ,    |          | 1 PAPK (17X); Similar to January 1 A41R, corresponds to Genbank     |                  | 1         |
|      |          |   |                  |           |
|      |          | Accession Number U17055 Paramecium bursaria Chlorella virus         | 57               | 26.667    |
| 6    | U42580   | Paramecium bursaria Chioretta                                       |                  | 1         |
| 0    | 0.22     | Paramecium bursaria chicare<br>1 PAPK (17X); similar to PBCV-1 ORF  |                  |           |
|      |          | AAID COrresponds to Gendam  |                  |           |
|      |          |   | 71               | 30.769    |
|      | U42580   |   | /-               |           |
| 8    | 042300   | l mr /17V), cimilar to FBCV I out                                   |                  |           |
|      |          |   |                  |           |
|      | 1        |   | 68               | 26.562    |
|      |          |   | 68               |           |
| 10   | U42580   |   |                  |           |
|      |          | 1 1 1 D COrresponds to Gendani                                      |                  |           |
|      | 1        |   |                  | 29.365    |
|      |          |   | 164              | 29.303    |
| 11   | U42580   | (19V), eimilar to PBCV-1 CM   | l                |           |
| _    | 1        | A41R, corresponds to Genbank  |                  |           |
|      |          |   |                  |           |
|      |          | Caenorhabditis elegans contains                                     | 206              | 29.240    |
| 12   | U80443   | caenorhabditis elegans contact similarity to a band 4.1-like        | 1                |           |
| 1    |          | similarity to a band 4.1 2200                                       | 1                |           |
| 1    |          | domain; Pfam domain PF00373   | 1                |           |
| 1    |          | (Band4_1) Score=132.4, E=8.4e-42,                                   |                  |           |
| 1    |          | N=1   | 148              | 32.911    |
| 13   | U80443   | Caenorhabditis elegans contains                                     |                  |           |
| 13   | 0000     | caenorhabditis elegans<br>similarity to a band 4.1-like             | 1                |           |
|      | 1        |   | 1                |           |
| 1    |          | (Band4_1) Score=132.4, E=8.4e-42,                                   | 1                |           |
| 1    |          | N-1   | 66               | 26.744    |
|      | AF149422 | Homo sapiens unknown  | 738              | 78.125    |
| 14   | AF149422 | Homo saniens unknown  | 1229             | 50.117    |
| 15   | AF149422 | Homo sapiens unknown  | 76               | 40.541    |
| 16   |          | Homo sapiens unknown  | 58               | 36.111    |
| 17   | AF149422 | Homo sapiens unknown  |                  | 30.769    |
| 18   | AF149422 | Homo sapiens unknown  | 60               | 82.353    |
| 19   | AF149422 | Homo sapiens unknown  | 102              | 20.588    |
| 20   | AF149422 | Homo sapiens unknown  | 67               |           |
| 21   | AF149422 | Homo sapiens wiknown  | 66               | 20.571    |
| 22   | AF149422 |   | 4623             | 25.256    |
| 23   | AF149422 | Homo sapiens unknown  | d 98             | 50.000    |
| 25   | L24521   | Homo sapiens transformation   |                  |           |
| 25   |          |   |                  | 29.474    |
| 1    | 1,24521  | protein Homo sapiens transformation-relate                          |                  |           |
| 26   | 124221   |   |                  | 71.765    |
|      | 704500   | Homo sapiens transformation-relate                                  | 31.4             |           |
| 27   | L24521   |   |                  | 63.855    |
| 1    |          | Protein Homo sapiens transformation-relat                           | ed 297           | 03.035    |

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TABLE 22

|        |          | i wakasam protein  | 2794 | 90.343 |
|--------|----------|--|------|--------|
| 801    | M22334   | Homo sapiens unknown protein   | 2108 | 92.793 |
| 802    | M22334   | Homo sapiens unknown protein   | 2695 | 85.804 |
| 803    | M22334   | Homo sapiens unknown protein   | 3731 | 92.707 |
| 804    | M22334   | Homo sapiens unknown protein   | 1213 | 91.753 |
| 5805   | U87306   | Rattus norvegicus transmembrane  |      |        |
| ,,,,,  |          | receptor UNC5H2  | 143  | 86.957 |
| 5808   | S58722   | Homo sapiens X-linked retinopathy                                      |      |        |
| 5000   |          | protein {C-terminal, clone XEH.8c}                                     | 143  | 86.957 |
| 5809   | S58722   | Homo sapiens X-linked retinopathy                                      | _    |        |
| 5005   |          | protein {C-terminal, clone XEH.8c}                                     | 4453 | 90.025 |
| 5810   | AL079292 | Homo sapiens hypothetical protein,                                     |      |        |
| 50     | \        | similar to (AC007017) putative RNA                                     | 1    |        |
|        |          | helicase A   | 5080 | 98.767 |
| 5811   | AL079292 | Homo sapiens hypothetical protein,                                     |      | 1      |
| 3011   |          | similar to (AC007017) putative RNA                                     |      |        |
|        |          | helicase A   | 253  | 97.297 |
| 5812   | AL079292 | Homo sapiens hypothetical protein,                                     |      |        |
| 30     |          | Homo sapiens hypothetical prive RNA similar to (AC007017) putative RNA |      |        |
|        |          | helicase A   | 163  | 59.184 |
| 5813   | U48830   | Mus musculus subtilisin-like   |      |        |
| 3020   |          | proprotein convertase  | 311  | 58.333 |
| 5814   | S58722   | Homo sapiens X-linked retinopathy                                      |      |        |
| 3021   |          | protein {C-terminal, clone XEH.8c}                                     | 237  | 74.545 |
| 5815   | S58722   | Homo sapiens X-linked retinopathy                                      |      |        |
|        |          | protein {C-terminal, clone XEH.8c}                                     | 3242 | 86.897 |
| 5816   | AB029008 | Homo sapiens KIAA1085 protein  | 3769 | 96.558 |
| 5817   | AB029008 | Homo sapiens KIAA1085 protein  | 2424 | 83.691 |
| 5818   | AB029008 | Homo sapiens KIAA1085 protein  | 764  | 82.432 |
| 5819   | AB029008 | Homo sapiens KIAA1085 protein  | 3446 | 95.431 |
| 5820   | AB029008 | Homo sapiens KIAA1085 protein  | 500  | 49.064 |
| 5822   | AF010144 | Homo sapiens neuronal thread   | 1    |        |
| 1 3322 |          | protein AD7c-NTP   |      |        |

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sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

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The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each,
20 unless the context dictates otherwise.

# 5.2 NUCLEIC ACIDS AND PEPTIDES OF THE INVENTION

Sequences of the nucleic acids and peptides of the present invention are set forth in the Sequence Listing. Table 1 relates the SEQ ID's listed herein to their identification in parent applications from which this application claims priority.

TABLE 1

| Gene   | Serial<br>Number         | Date<br>Filed                 | SEQ ID NO. in Parent Applications          | SEQ ID NO:<br>in Current Application | File Name<br>On CD |
|--------|--------------------------|-------------------------------|--|--------------------------------------|--------------------|
| Family | Number                   |                               |  | 748 SEQ ID NO: 1-45,196              | N/A                |
| 748    | 09/205,070<br>09/340,623 | Dec. 3, 1998<br>Jun. 28, 1999 | SEQ ID NO: 1-45,196<br>SEQ ID NO: 1-45,196 | 748 SEQ ID NO: 1-45,196              |                    |

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| Da    | ate of Deposit: Februa   | 1 9 20, 200-          |                         |                                    |
|-------|--------------------------|-----------------------|-------------------------|------------------------------------|
|       |                          | SEQ ID NO: 1-45,196   | 748 SEQ ID NO: 1-45,196 |                                    |
| 0     | 9/898,888 Jul. 3, 2001   | SEQ ID No. 1          |                         | N/A                                |
|       |                          | SEQ ID NO: 1-13192    | 752 SEQ ID NO: 1-13192  |                                    |
| 752   | 19/205,155 Dec. 3, 1998  | SEQ ID NO. 1-13192    | 752 SEQ ID NO: 1-13192  | l                                  |
|       | 09/359,922 Jul. 22, 1999 | SEQ ID NO: 1-13192    | 752 SEQ ID NO: 1-13192  | 1                                  |
|       | 09/919,002 Jul. 30, 2001 | SEQ ID NO: 1-13192    | 132 3 - 2               | 37/4                               |
|       | ****                     |                       | 778 SEQ 1D NO: 1-94     | N/A                                |
|       | 09/347,127 Jul. 2, 1999  | SEQ 1D NO: 1-94       | 778 SEQ 1D NO: 1-94     |                                    |
| 778   | 09/905,059 Jul. 12, 2001 | SEQ ID NO: 1-94       | 118 SEQ ID ITO          | l                                  |
|       | 09/903,037 34, -         |                       |                         | N/A                                |
|       | 09/457,877 Dec. 8, 1999  | SEQ ID NO: 1-128      | 779 SEQ ID NO: 1-128    | 1                                  |
| 779   | 09/457,877 Dec. 6, 1999  | SEQ ID NO: 1-128      | 779 SEQ 1D NO: 1-128    |                                    |
|       | 09/952,981 Sep. 14, 2001 |                       |                         | Table2(782).doc                    |
|       |                          | SEQ ID NO: 1-10,451   | 782 SEQ ID NO: 1-10,451 |                                    |
| 782   | 09/471,275 Dec. 23, 1999 | SEQ ID NO. 1 17       |                         |                                    |
|       |                          | SEQ ID NO: 1-10289    | 784 SEQ ID NO: 1-10289  | Table3(784).doc; Table4(784).doc   |
| 784   | 09/488,725 Jan. 21, 2000 | SEQ ID NO. 1-10209    | 784 SEQ ID NO: 1-10289  | Tables (784) coo, Tables           |
|       | 09/552,317 Apr. 25, 2000 | SEQ ID NO: 1-10289    |                         | (Table 5 and 7 are hard copies)    |
|       |                          |                       | 785 SEQ ID NO: 1-3796   | Table 6 (785).doc                  |
| 785   | 09/491,404 Jan. 25, 2000 | SEQ ID NO: 1-3796     | 785 SEQ ID NO: 1-3796   | Tableb(783).doc                    |
| 1 ,03 | 09/922,279 Aug. 3, 2001  | SEQ ID NO: 1-3796     | 165 SEQ 1-              | = 11 0/797) doc                    |
|       | 0)//22,217               |                       | 787 SEQ ID NO: 1-3960   | Table8(787).doc; Table9(787).doc;  |
|       | 09/496,914 Feb. 23, 2000 | SEQ ID NO: 1-3960     | 787 SEQ ID NO: 1-3960   | Table10(787).doc                   |
| 787   | 09/560,875 Apr. 27, 2000 | SEQ ID NO: 1-3960     | 787 SEQ ID NO. 1-3700   |                                    |
| 1     | 09/300,673 74/1.27       |                       | 17 270 1 14074          | Table11(788).doc; Table12(788).do  |
| 1     |                          | SEQ ID NO: 1-14074    | 788 SEQ ID NO: 1-14074  | Table13(788).doc                   |
| 788   | 09/515,126 Feb. 28, 2000 |                       | 788 SEQ ID NO: 1-14074  |                                    |
| 1     | 09/577,409 May. 18, 200  | 0 5=4                 |                         | Table14(789).doc; Table15(789).do  |
| 1     |                          | SEQ ID NO: 1-6391     | 789 SEQ ID NO: 1-6391   | Table 16(789).doc                  |
| 789   | 09/519,705 Mar. 7, 200   |                       | 789 SEQ ID NO: 1-6391   |                                    |
| 1     | 09/574,454 May. 19, 2000 | 00 SEQ ID NO. 1 see   |                         | Table17(790).doc; Table18(790).d   |
| 1     |                          | 00 SEQ ID NO: 1-30533 | 790 SEQ ID NO: 1-30533  | Table19(790).doc                   |
| 790   | 0 09/540,217 Mar. 31, 20 | 20522                 |                         | 1401015(150).                      |
| 1 "   | 09/649,167 Aug. 23, 20   | 00 SEQ 1D NO: 1-30533 |                         | Table20(791).doc; Table21(791).    |
| 1     |                          |                       | 791 SEQ ID NO: 1-5822   | Table20(791).doc, Table22(791).doc |
| 79    | 1 09/552,929 Apr. 18, 20 | 00 SEQ ID NO: 1-5822  | 10. 1 5922              | Table22(791).doc                   |
| 1 "   | 09/770,160 Jan. 26, 20   | 01 SEQ ID NO: 1-5822  | 171 000 10 110          |                                    |
| 1     | V// /                    |                       | 792 SEQ ID NO: 1-8502   | (Table 23-25 are hard copies)      |
| 1     | 92 09/577,408 May. 18, 2 | 000 SEQ ID NO: 1-8502 | 192 SEQ ID 110. 1       |                                    |

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of 748 SEQ ID NO: 1-45,196, 752 SEQ ID NO: 1-13,192, 778 SEQ ID NO: 1-94, 779 SEQ ID NO: 1-128, 782 SEQ ID NO: 1-10,451, 784 SEQ ID NO: 1-10,289, 785 SEQ ID NO: 1-3796, 787 SEQ ID NO: 1-3960, 788 SEQ ID NO: 1-40,74, 789 SEQ ID NO: 1-6391, 790 SEQ ID NO: 1-30,533, 791 SEQ ID NO: 1-5822, and 792 SEQ ID NO: 1-8502; a polynucleotide encoding any one of the peptide

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### **EXAMPLES**

6.0 Selected tables are provided on the CD-ROM, supplied concurrently with this application. The entirety of the contents of the CD-ROM are intended to be a part of this application, and are incorporated by reference. The electronic file name, where appropriate, follows the first reference to the table throughout the application.

#### The 748 Gene Family 6.1

## **Novel Contigs**

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The novel contigs of the invention, were assembled from novel expressed sequence tags (EST's) isolated by methods described herein (e.g., SBH), and in some cases sequences obtained from one or more public databases. The inserts for the cDNA libraries from which the novel ESTs were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts. These samples were spotted onto nylon membranes and interrogated with oligonucleotide probes to give sequence signatures. The clones were clustered into groups of similar or identical sequences, and single representative clones were selected from each group for gel sequencing. The 5' sequence of the amplified inserts was then deduced using the reverse 15 M13 sequencing primer in a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel ESTs. The novel contigs of the invention, were assembled from the novel ESTs 20 and, in some cases, sequences obtained from one or more public databases. The sequences for the resulting contigs from the 748 gene family are designated as 748 SEQ ID NO: 1-45,196 and are provided in the Sequence Listing.

#### The 752 Gene Family 6.2 25

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## Novel Contigs

The novel contigs of the invention, were assembled from novel expressed sequence tags (EST's) isolated by methods described herein (e.g., SBH), and in some cases sequences obtained from one or more public databases. The inserts for the cDNA libraries from which the novel ESTs were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts. These samples were

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libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The inserts for the cDNA libraries from which the sequences were obtained were amplified with PCR using primers specific for the vector sequences which flank the inserts, or isolated from plasmid preparations. The 5' sequence of the amplified inserts was then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol, as well as internal primers in both the forward and reverse direction. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction. In all cases all of a signature cluster was sequenced to generate overlapping clones to assemble the contigs. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three applications designated PHRED, PHRAP, and CONSED. The sequences for the resulting contigs for the 782 gene family are designated as 782 SEQ ID NO: 1-10,451 and are provided in the attached Sequence Listing. inserts was then deduced in a typical Sanger sequencing protocol. The inserts of the library were, amplified with PCR using 5 primers specific for vector sequences which flank the inserts. 15

The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 782 SEQ ID NO: 1-10,451 are shown in Table 2, and identified as Table2(782).doc on the enclosed compact disc.

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#### The 784 Gene Family 6.6

## Novel Contigs

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Table 3 (identified as Table3(784).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (784 SEQ ID NO: 1-10,289) of the present invention, and their corresponding nucleotide locations to each of 748 SEQ ID NO: 1-10,289. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a 15 polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. When the predicted beginning nucleotide of Table 3 is a higher number than the predicted end nucleotide of Table 3, then the amino acid sequence is derived from the 20 complementary strand of the indicated SEQ ID NO. The locations of the predicted beginning and end nucleotides correlate to the nucleotide sequence of the indicated SEQ ID NO., not its complementary strand.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 3 or from six frame translations of 784 SEQ ID NO: 1-10,289; or the corresponding full length or mature protein. One of skill in the art could determine the corresponding amino acid sequence using techniques well known in the art to translate and analyze all possible six frames. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the 784 SEQ ID NO: 1-10,289; or (b) polynucleotides that hybridize to the

Table 4 (identified as Table4(784).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 784 SEQ ID NO: 1-10,289).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 784 SEO ID NO: 1-10.289 are shown in the Table 5. infra.

#### 6.7 The 785 Gene Family

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#### Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described above, and in some cases sequences obtained from one or more public databases. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three

applications designated PJRED, PHRAP, and CONSED. The sequences for the resulting contigs are designated as 785 SEQ ID NO: 1-3,796 and are provided in the Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using Fastxy algorithm. Fastxy is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 785 SEQ ID NO: 1-3,796 are shown in Table 6 (identified as Table6(785).doc on the enclosed CD), infra.

The nucleotide sequence within the assembled contigs that codes for signal peptide sequences and their cleavage sites can be determined from using Neural network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptidesand their cleavage sites are also disclosed iby Henrick Nielson, Jacob Englebrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, vol. 10, no. 1, pp. 1-6 (1997) incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et. al., reference, are obtained from each assembled contig. Table 7 sets forth the nucleotide sequence range for each sequence of 785 SEQ ID NO: 1-3,796 that encodes a corresponding forty-five amino acid sequence containing the signal peptide sequence and its cleavage site, the maximum S score and the mean S score obtained for each sequence. Not all forty-five amino acids in the sequence may comprise the signal peptide.

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#### The 787 Gene Family 6.8

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Table 8 (identified as Table8(787).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (787 SEQ ID NO: 1-3960) of the present invention, and their corresponding nucleotide locations to each of 787 SEQ ID NO: 1-3960. Table 8 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated 10 herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a 15 polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. When the predicted beginning nucleotide of Table 8 is a higher number than the predicted end nucleotide of Table 8, then the amino acid sequence is derived from the 20 complementary strand of the indicated SEQ ID NO. The locations of the predicted beginning and end nucleotides correlate to the nucleotide sequence of the indicated SEQ ID NO., not its complementary strand.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 8 or from six frame translations of 787 SEQ ID NO: 1-3960; or the corresponding full length or mature protein. One of skill in the art could determine the corresponding amino acid sequence using techniques well known in the art to translate and analyze all possible six frames. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the 30 787 SEQ ID NO: 1-3960; or (b) polynucleotides that hybridize to the complement of the

into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 9 (identified as Table9(787).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 787 SEQ ID NO: 1-3960).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 114, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 787 SEQ ID NO: 1-3960 are shown in the Table 10, (identified as Table10(787).doc on the enclosed CD) infra.

#### 6.9 The 788 Gene Family

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Table 11 (identified as Table11(788).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polypucleotides (788 SEO ID NO: 1-14,074) of the present invention, and their corresponding nucleotide locations to each of 788 SEQ ID NO: 1-14,074. Table 11 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of translated novel polypucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame. When the predicted beginning nucleotide of Table 11 is a higher number than the

Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

#### **Novel Contigs**

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting contigs are designated as 788 SEQ ID NO: 1-14,074 and are provided in the attached Sequence Listing; The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 12 (identified as Table12(788).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 788 SEQ ID NO: 1-14,074).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 788 SEQ ID NO: 1-14,074 are shown in the Table 13, (identified as Table13(788).doc on the enclosed CD) infra.

#### 6.10 The 789 Gene Family

Table 14 (identified as Table14(789).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (789

SEQ ID NO: 1-6,391) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 1-6,391. Table 14 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

Novel Contigs

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The novel contigs or the nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting contigs are designated as 789 SEQ ID NO: 1-6,391 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UriGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95 %.

Table 15 (identified as Table15(789).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 789 SEQ ID NO: 1-6,391).

The nearest neighbor result far the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 789 SEQ ID NO: 1-6,391 are shown in the Table 16, (identified as Table16(789).doc on the enclosed CD) infra.

6.11 The 790 Gene Family

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Table 17 (identified as Table 17(790).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (790 SEQ ID NO: 1-30,553) of the present invention, and their corresponding start and stop nucleotide location to each of 790 SEQ ID NO: 1-30,553. Table 17 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide

database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 10.3, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there were no additional sequences from the databases that will extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 18 (identified as Table18(790).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 790 SEQ ID NO:1-30,553).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 1.15, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 790 SEQ ID NO: 1-30,553 are shown in the Table 19, (identified as Table19(790).doc on the enclosed CD) infra.

#### 6.12 The 791 Gene Family

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Table 20 (identified as Table20(791).doc on the enclosed CD) sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (791 SEQ ID NO: 1-5,822) of the present invention, and their corresponding nucleotide locations to each of 791 SEQ ID NO: 1-5,822. Table 20 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J.

Table 21 (identified as Table21(791).doc on the enclosed CD) shows the various tissue sources of the EST sequences from Hyseq's database which were used to assemble the contigs or nucleic acids of the present invention (identified by 791 SEQ ID NO: 1-5.822).

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 115, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for 791 SEQ ID NO: 1-5,822 are shown in the Table 22, (identified as Table22(791).doc on the enclosed CD) infra.

#### 6.13 The 792 Gene Family

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Table 23 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (792 SEO ID NO: 1-8,502) of the present invention, and their corresponding nucleotide locations to each of 792 SEO ID NO: 1-8,502. Table 23 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), incorporated herein by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268: 78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in Table 23 or from six